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(54) Title: CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon
5 programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

Invasive fungal infections (e.g. *Candida* spp, *Aspergillus* spp., *Fusarium* spp.,
10 *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal
15 infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of
20 unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botritis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is
25 thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism.
30 These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

Cells from multicellular organisms can commit suicide in response to specific
35 signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. To

survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has been assumed that such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a
5 similar process of cell survival also operates in single-celled eukaryotes.

It has been found that expression of the mammalian *Bax* gene triggers cell death in *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* with morphological changes similar to apoptosis (Jürgensmeier *et al.*, 1997). However, the mechanism of *Bax* lethality in *S. cerevisiae* remains unclear.

10 Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes.

It is an aim of the present invention to provide nucleic acid as well as
15 polypeptide sequences which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases
20 associated with yeast or fungi.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

25 It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in yeast
30 or fungi infections. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds.

It is also an aim of the invention to provide a method of preventing infection with yeast or fungi.

It is also an aim of the invention to provide probes and primers derived from the
35 nucleic acid sequences of the invention.

All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. As explained in Example 2, genes showing a difference of a factor 5 or more in expression as a result of *Bax*-induced cell death, were identified as differentially expressed candidate genes. Some of these genes are clearly down-regulated in a *Bax*-expressing strain, while other genes show an upregulated expression (Table 1). Example 3 describes a further experiment wherein the results of differential expression were analysed using the PathwaysTM software and differentially expressed nucleic acid sequence were identified.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more

- preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e); and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using
5 BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide
10 or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to
15 determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine
20 identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15,
25 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
30 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473 .

The invention also relates to nucleic acid sequences from *Candida albicans*, as represented by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303,
35 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,

373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides.

Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483; and,
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f).
- According to a more specific embodiment, these nucleic acid sequences are derived from *Saccharomyces cerevisiae*, *Candida albicans* or *Aspergillus fumigatus*.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook et al., 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The term "nucleic acid sequence" also includes the complementary sequence
5 to any single stranded sequence given, or the antisense version thereof.

The invention also relates to mRNA, DNA or cDNA versions of the nucleic acid molecules of the invention.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined
10 nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid sequences of
15 at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically
20 with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under
25 hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto
30 the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR
35 cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be

cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined
5 herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme
10 labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a
15 suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be
20 a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the
25 invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

30 Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and
35 fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2,
5 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48,
50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,
94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126,
128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158,
160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
10 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222,
224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286,
288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,
320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350,
15 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382,
384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414,
416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446,
448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478,
480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of
20 said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar,
preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid
sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28,
25 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72,
74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112,
114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144,
146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,
178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
30 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240,
242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,
274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304,
306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336,
338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368,
35 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400,
402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75,
5 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106,
10 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276,
15 278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474. Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378,
20 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative
25 amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant)
30 nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as
35 proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids,

amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may
5 also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections
10 caused by yeast or fungi.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

15 According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the
20 invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds may carry agonistic or antagonistic properties. The compounds to be screened may be of extracellular, intracellular, biologic or chemical origin.

Such a screening method may comprise the following steps (a) contacting a
25 compound to be tested with cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated cells is indicative of selective action of said
30 compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively
35 monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

The term "cells" as used above relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein

differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps:

incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence

according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose

will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, abd even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughput assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting, band-shift, co-

immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein trageting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Yersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for
5 altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing
10 and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughout assays.

In cases compounds need to be found to target tumor cells, screening assays
15 will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds
20 identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

25 According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

The invention also relates to a compound identified using any of the methods of the invention.

30 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

35 The compounds of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections,

for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
5 and *Sporothrix schenckii* infections.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungistatic
10 compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids or polypeptides of the invention, which overexpression or
15 underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

20 Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi
25 selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394,
30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90 or
35 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,

306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452
5 454, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 75% or 80% identical, more preferably more than 85%, 90%
or 95% identical and most preferably more than 97% identical to any of the amino
acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302,
10 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342,
344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376,
380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416,
418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450,
452, 454, 476, 478, 480, 482, or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as
a medicament.

Also encompassed within the present invention are antibodies, monoclonal or
polyclonal, capable of specifically binding to one or more epitopes of the proteins of the
20 invention. The term "specific binding" implies that there is substantially no cross-
reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to
techniques which are known to those skilled in the art. Monoclonal antibodies may be
prepared using conventional hybridoma technology as described by Kohler and
25 Milstein (1979). Polyclonal antibodies may also be prepared using conventional
technology well known to those skilled in the art, and which comprises inoculating a
host animal, such as a mouse, with a protein or epitope according to the invention and
recovering the immune serum. The present invention also includes fragments of whole
antibodies which maintain their binding activity, such as for example, Fv, F(ab') and
30 F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of
detecting the presence of a polypeptide according to the invention, which method
comprises reacting the antibody with a sample and identifying any protein bound to
said antibody. A kit may also be provided for performing said method which comprises
35 an antibody according to the invention and means for reacting the antibody with said
sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to,
5 *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium* spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

10 According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic
15 acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art
20 (Sambrook et al., 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides
25 of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

The invention further relates to the compounds identifiable according to the above-described method and its use as a medicament.

The invention further relates to a method for preparing a pharmaceutical
30 composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate
35 due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal

benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases
5 such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

10 According to another embodiment, the invention relates to the use of a nucleic acid molecule or a polypeptide described in the invention or human homologues thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention also relates to a pharmaceutical composition for use as a
15 medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

The invention also relates to a vaccine for immunizing mammals against
20 proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically acceptable carrier.

The invention also relates to the use of an antibody of the invention capable of
25 binding to at least one of the polypeptides of the invention or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention.
30 Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

According to another embodiment the invention relates to a nucleic acid
35 molecule comprising a human homologue of at least one of the nucleic acid sequences described in the invention.

The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

5 The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the invention.

10 The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

- Figure 1.** *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)
- Figure 2.** *Candida albicans* sequences (SEQ ID Nos 285 to 456).
- 5 **Figure 3.** Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.
- 10 The spots represent the genome wide expression profile without (A) and with (B) *Bax* modulated expression (Example 2).
- Figure 4.** Results from a second experiment analogous and analysed as described in the examples section (Example 3).
- 15 **Table 1.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed more than fivefold in a first experiment (see Example 2). The factor by which the transcript level was affected, is expressed as the Qt value. A Qt value higher than 1 indicates upregulation while a Qt value lower than 1 indicates a
- 20 downregulation. For instance, a Qt of 0.5 indicates a two-fold lower transcript level of a particular mRNA due to *Bax* expression in *S. cerevisiae*. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0.21, respectively.
- 25 **Table 2.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly in a second experiment (see Example 3). In this experiment, the Qt values were calculated using the Pathways Software (Research Genetics).

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was
5 used for the construction and the amplification of plasmids. Yeast strains were grown
under normal conditions on standard media (Sherman *et al.*, 1979). The
Saccharomyces cerevisiae strain INVSc1 (Invitrogen®) was transformed by means of
the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTyLMuBax,
after linearisation in the Ty δ element (Zhu, 1986).

10

Cloning of mouse BAX cDNA

Mouse *Bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA
polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18
thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

15

5'-ATGGACGGGTCCGGGAGCAG-3' and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to
standard procedures (Sambrook J. *et al.*, 1989).

20

Plasmid constructions

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI-HindIII* GAL1
promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI* FLP
terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that
25 the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in
the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent
insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-
openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse *Bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII*
30 and subcloned into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final
expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP culture
collection as p5CTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

5 The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

10 Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

15 The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains
20 the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

25

Results***Induction of Bax-expression in yeast cells***

30 *S. cerevisiae* cells (strain INVSc1) were transformed with the expression plasmid YIpUTyLMuBax or the parental plasmid YIpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

The Ty δ element of both plasmids allowed a stable multi-copy integration in the genome of the yeast cell. Southern analysis of the cells containing YIpUTyLMuBax
35 revealed the integration of 5 GAL1-controlled Bax-cassettes near Ty elements.

The yeast cells containing YIpUTyLMuBax and the yeast cells containing YIpUTyL were grown overnight in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD₆₀₀ of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells containing YIpUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD₆₀₀ of 1. The yeast cells containing YIpUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

RNA isolation

Total RNA was isolated using RNAPure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 · 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH₂O.

First strand cDNA synthesis in the presence of α-³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL yeast cells and incorporation of α-³³P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

- 6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)
- 1 µl 0,1 M DTT
- 1 µl RNase Block (40 units/µl) (Stratagene)
- 1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)
- 1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
- 10 µl α-³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid
5 scintillation. The specific activity of the probes was 3 or 5 10^8 cpm/ μ g for both the INVSc1YIpUTyL and the INVSc1YIpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the
10 detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α - 32 P dCTP
15 labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during
20 prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 or 10 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (0,5 or 1 μ g/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating.
25 Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from
30 Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

Example 2. Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

Statistical processing of quantification results

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.
2. The frequency in terms of percentage.
3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

Subsequently, the results of the two experiments (hybridization with cDNA from YlpUTyL containing INVSc1 cells and hybridization with cDNA from YlpUTyLMuBax containing INVSc1 cells) were integrated by determination of a second range of statistical functions:

1. The average of the values of the two experiments for each spot on the filter.
2. The standard deviation on this average. This is a measure for the distribution of the values around this average.
3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately gave the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of percentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially expressed candidate gene. (Table 1).

Requantification of these candidates confirmed their selection.

When the expression pattern of all 6144 genes is compared in the two experiments, it could be concluded that the expression profile of 142 genes (this is 2,3 %) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1. The sequences of these genes and the amino acid sequences which they encode are shown in Figure 1.

Example 3 . Quantification of Hybridisation Signals using the Pathways™ software

Quantification of the hybridisation signals was done using the Pathways™ Software (Research Genetics) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 2.

Surprisingly, using this Software package for analysing the results in this example and when compared to the results of example 2, some additional genes were found which expression are up-or down-regulated upon *Bax* expression in *S. cerevisiae*.

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

Example 4 Search for homologues in *Candida albicans*

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

Example 5 . Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; 5 Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to 10 the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally 15 sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test 20 compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti- 25 sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

30 **Example 6. Assay for High Throughput screening for drugs**

35 $35\ \mu\text{l}$ minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers $2.5\ \mu\text{l}$ of R-compound at $10^{-3}\ \text{M}$ in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with 20 $\mu\text{g/ml}$ uridine. A single colony is scooped
5 up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml.
10 Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

200 μl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

15 Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Table 1.

ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103

YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211

YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Table 2.

ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

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CLAIMS

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which
5 nucleic acid sequence is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

- 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,

- 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; and
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to f),
- for the preparation of a medicament for treating diseases associated with yeast or fungi.

2. Use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c),
for the preparation of a medicament for treating diseases associated with yeast or fungi.

25

3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

30

4. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid molecule as defined in claim 1 or at least one polypeptide as defined in claim 2 in a pharmaceutically acceptable carrier.

35

5. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or

underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.

5 6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

10 (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,

15 (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

20 (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

25 7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

30 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,

35 (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is

indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- 5 (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 10 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

8. A method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

15

- (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,
- (b) detecting the complex formed between the compound to be tested and said polypeptide,
- 20 (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound being tested.
- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

25

9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- 30 (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
- (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.
- 5 11. A compound identifiable according to the method of any of claims 6 to 9.
12. A compound according to claim 11 for use as a medicament.
- 10 13. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.
14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.
- 15 15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
- 20 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
25 and *Sporothrix schenckii*.
17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- 30 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
35 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 10 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 15 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 20 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 25 (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- 30 (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 35 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e).

5 18. A nucleic acid according to claim 16 characterized in that it is derived from *Candida albicans*.

 19. A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.

10

 20. A nucleic acid sequence according to any of claim 17 to 19 which is mRNA

 21. A nucleic acid sequence according to any of claims 17 to 19 which is
15 DNA.

 22. A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.

20 23. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.

 24. An isolated protein which is involved in a pathway for programmed cell
25 death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and
35 most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

- 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 5 (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 10 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484; and,
- 15 (d) a functional fragment of any of said proteins as defined in a) to c)
25. An expression vector comprising a nucleic acid sequence according to any of claims 17 to 23 .
- 20 26. An expression vector according to claim 25 which comprises an inducible promoter.
27. An expression vector according to claim 25 or 26 which comprises a sequence encoding a reporter molecule.
- 25 28. A host cell transformed, transfected or infected with the vector of any of claims 25 to 27.
29. A nucleic acid molecule according to any of claims 17 to 23 for use as a 30 medicament.
30. A polypeptide according to claim 24 for use as a medicament.
31. An antibody capable of specifically binding to a polypeptide according to 35 claim 24.

32. An antibody according to claim 31 for use as a medicament.

33. A pharmaceutical composition comprising an antibody according to claim 31 or 32.

5

34. Use of an antibody according to claim 31 or 32, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation of a medicament for treating diseases associated with yeast and fungi.

10

35. Use of an antibody according to claim 34 where the fungus is *Candida albicans*.

15

36. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively hybridises with any of said nucleic acid molecules.

20

37. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively amplifies any of said nucleic acid molecules.

25

38. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or a human homologue thereof or at least one of the polypeptides as defined in claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

30

39. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences as defined in claim 1 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

35

40. A compound identifiable according to the method of claim 39.

41. A compound according to claim 40 for use as a medicament.

42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising
5 admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain
10 disorders.

44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
15

45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.
20
25

47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.
30

48. Use of an antibody according to claim 31 or 32 or an antibody capable of binding to at least one of the polypeptides as defined in claim 2 or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
35

49. An expression vector comprising a human homologue of a nucleic acid sequence as defined in claim 1.

50. An expression vector according to claim 49 which comprises an inducible promoter.

5

51. An expression vector according to claim 49 or 50 which comprises a sequence encoding a reporter molecule.

52. A host cell transformed, transfected or infected with the vector of any of claims 49 to 51.

10

53. A nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences as defined in claim 1.

15

54. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 53.

55. A polypeptide encoded by a nucleic acid molecule according to claim 53.

20

FIG. 1:

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)

AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGGAGTTCTCAAGACTTATACTT
CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTCGTTACAACGTCTGCAGGACTCTT
TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAAATGTGGTTGTAACCTTTT
TAATTTTTTTCTTGAACCTGTTGAGTCGTAATAATCGTTTCTGGGAAGTGAAGGTAAT
AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAAGTGTGTAGG
GACGTTTCGATACCAAAATTTCTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT
CGTAGCGCATACATCTGATCGAAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC
CAGCATCAAAATTTTCATCATTAAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA
CCTGATTGACGAACCAAGAAATGCCTTATCACTATTTATTTTTTGGCACTCTTCACCTACC
TGGCCACGTCCAATGTTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGGGCCCCGAGGA
AAAATGGGATGAATGTCAACTTTTATAAATCACTATTACTGGATTCAACAACGTATTCCT
ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)

MPYHYLFALFITYLATSNVVSSTQACLPVGPRKNGMNVNFYKYSLLDSTTYSYPQYMTS
GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)

AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA
AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTATTCAAGATTATTGGTTTTTC
CTAACCGCCGCGCCGCGCAGGTACCCCGCGCATCTCTTCTCTCGAAGAAAGCGGAAAAA
ACAAAAAAGTATAAATAGTGGAGTCTTTTCCCATTTAACATTTAGAAAAAATTCG
AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCCTTGGCGGCTTTTTCTCAGTTTCG
TGGGCTAGTACATTTACCTAGTATGCTGGGAACTTTTTTTCCGTATTCTATTCTATTCC
TTGCCTTACTTTTCTTATCATTTTTTATATAACCAATTTCAAAAATACTTTTAACTGTC
ATAGACGCATTTTGTATTATTACAAATTAAGAATCAAAATATAATATGTGCAATTAATAA
CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA
CCAAGAGCCTACCAAGACCGGATGGTTTGTGTCAGTGCAGGAAGTATGGACTCCAAGATCA
GAGGTGGGTGGCTTATAACGATTTTTTAATCTTACCAGGTTTAGTCGATTTTGCCTCCT
CTGAAGTTAGCCTACAGACCAAGCTAACCAGGAATATTACTTTAAACATTCCATTAGTAT
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTATGGCTCTGTTGGATG
GTACCTGTTTCACTCACCATAACTGTACTCCAGAGGACCAAGCTGACATGGTCAGAAAG
TCAAGAAGTATGAAAATGGGTTTATTAACAACCTATAGTGATTTCTCCAACACGACCG
TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTTGCAGGCTTCCCTGTCACGGCAG
ATGGAAAGAGAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG
AGGACAACCTCTTACTCGTTCAGGATGTGATGACCAAAAACCCTGTTACCGGCGCACAAG
GTATCACATTATCAGAAGGTAACGAAATTTCAAAGAAAATCAAAAAGGGTAGGCTACTGG
TTGTTGATGAAAAGGTAAGTACTAGTTTCTATGCTTTCCCGAACTGATTTAATGAAAAATC
AGAAGTACCCATTAGCGTCCAAATCTGCCAACCAAGCAACTGTTATGGGGTGCTTCTA
TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG
TCGTATATTTGGATTCCCTCTCAAGGTAAGTCTATTTTCCAATTGAACATGATCAAAATGGA
TTAAAGAAACTTTCCAGATTGGAATCATTGCTGGTAACGTTGTCACCAAGGAACAAG
CTGCCAATTTGATTGCTGCCGGTGCGGACGGTTTGAGAATTGGTATGGGAAGTGGCTCTA
TTTGTATTACCCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG
TGTGTGAATTTGCTAACCAATTCGGTGTTCATGTATGGCTGATGGTGGTGTTCAAAAAC
ATTGGTCATATTATTACCAAGCTTTGGCTCTTGGTCTTCTACTGTTATGATGGGTGGT
ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)

MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGLAYNDFLILPGLVDFASSEVSLQT
KLTRNITLNIPLVSSPMDTVTESEMATFMALLDGI GF IHNCTPEDQADMVRRVKNYENG
FINNPVIVISPTTVGEAKSMKEYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV
QDVMTKNPVTGAQGITLSEGNEILKKIKKGRLLVVDEKGNLVSMLSRTDLMKNQKYPLAS
KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVVILDSSQNSIFQLNMIKWIKETFPD
LEIIAGNVVTKQAANLIAAGADGLRIGMGTSICITQKVMACGRPQGTAVYNVCEFANQ
FGVPCMADGGVQKHWSYYYQSFSGSWFFYCYDGWYVGRYYRITR

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)

GGGAGAAGCTTATCTTACTGTAGAAGAAAATGGGATTGCGTTACTCCATATATATTGAAA
ATCCGTTATCTTCCCCATCATCATCGTATAAATCAATAAACGACCCGTTATTCCACTCTC
AGCATCGATCGCAAAAAAACGTGAGCTTCATCACCTACGGTTGTAGACATTGCAAGACAC
ATCTTTCAGTTCTTCCAGATTATTTCTAGAGATTATAGGGGTAGGACCGGAACGTGCTT
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTGAGCAACGAAGAATGTTGA
CTGGCGACTACTTAGTCTGTGATATCTTTTGTGCTATTGGTGCAAGAGGAACGTAGGTTGGA
AATACTTGCAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC
TGAAAAACATTTGTAAATGTACTTGATGTCTTCCTTTGTCTGCTATCTAGCACCTCTCGT
CTTTTAGTGCTTTTTTAGCGTATGATTCTTTTTAAGAATCTGGTCTTCTTCCCTTCTATTT
TGATTGGGTATATTTCTATTCGTGTTTCATTACTGGTCTGGGTAAATTGGGTTTTGGTTTT
GGTCCAGTTGTTTTCAAGTAGCCTTTATTTTTTTCATTGTGGTATTTATCTTATCGATTT
ATACTTTTTTTTTATTCAAAGAAAATTAACAGATAATCTCTTATGAGCCTAGCTACTTTG
TTTTTCTTACAGGGCCATTGACTTATGCCCTGAACGAGTCTTACTTTACTTTTTTTGTAA
TTTTCAATAATGTCGTGTTTCCCATGTTGTAA

YBL048W, 103 aa (SEQ ID NO 6)

MILFKNLVFLPSILIGYISIRVSLVWVNWVLVWSSCFQVAFIFSLWYFILSIYTFYFSK
KIKQIISYEPSYFVFSYRAIDLCPERVLlyFFCIFNNVFPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)

GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTACGGAATCA
CATAGCTTTTCATTTTGTTCCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC
TACAGGGTCTGACATTTTTAACTTTCAGGTTAATGATGGTGTCTTACTATATTTCTCGAG
TCGTACAGAAGTTAGTTCAGATAAACTGCTTCGGTGTCTGCCACTTCTTATCATTACTTC
AACTTTACCTTCCCTATACCTGTGTCTCCTTTATTAATTCAAGTTAATCCGAGGTAATAGA
TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTTCCT
GGAAAAGAATAACAATTAAGGCAGCCTTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA
TTAGCGCAAGAAGAAGTGTGATATAGTACTCATAGAGGCAGGCTACAGACTAGGGAAAGC
GTGTTCAACAACAATAAGAAATGGAGACCAGTTCTTTTGAGAATGCTCCTCCTGCAGCCA
TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC
AATCTATCGAAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAACGGAAACTGGTG
AGAACTCTGCAAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA
CCAATGGTGCTTTTGACGATGATGTTATCCCAAATGCTATTGTTATTTAAAAACATTTCCGT
TTGCTATTA AAAAGAGCAATTGTTAGACATTATTGAAGAAATGGATCTTCCCTTCTCTT
ATGCCTTCAATTACCACTTTGATAACGGTATTTTCAGAGGACTAGCCTTTGCGAATTTCA
CCACTCCTGAAGAACTACTCAAGTGATACTTCTTTGAATGGAAAGGAAATCAGCGGGA
GGAAATTGAAAGTGGAATATAAAAAAATGCTTCCCCAAGCTGAAAGAGAAAGAATCGAGA
GGGAGAAGAGAGAGAAAAGAGGACAATTAGAAGAACACACAGATCGTCATCTAATCTTT
CTTTGGATTCTTTATCTAAAATGAGTGAAGCGGAAACAATAATACTTCTAACAATCAAT
TATTCTCGACTCTAATGAACGGCATTAATGCTAATAGCATGATGAACAGTCCAATGAATA
ATACCATTAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTTCTGAACCAAC
CTTCACTTTCTGCCCAACATACTTCTTCATCGTTGTACCAAACAAACGTTAATAATCAAG
CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTTGCCTCTCC
CACCCCAACAACTGGACTTCAATGACCTGACACTTTTGGAATTTATTCCCAATTATTGT
TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT
CCCACAAGAGAATTATCAATGTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC
CAAGATTTTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGCG
AACAACAAGGTCAAATGACATCTGCTCATCCTTTGCGAGCCAACTCCACTGGCGGCTCCA
TGAATAGGTCACAATCTTATACAAGTTTGTACAGGCCCATGCAGCAGCTGCAGCGAATA
GTATTAGCAATCAGGCCGTAAACAATCTTCCAACAGCAATACTATTAACAGTAATAACG
GTAACGGTAACAATGTCATCATTAATAACAATAGCGCCAGCTCAACACCAAAAATTTCTT
CACAGGGACAATTTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA
GTTCTCAATACAATTCGCGAGACCAACCGCAACAACCTCAACCACAAACACAGCAAAATG
TTCACTCAGCTGCGCAACAACAACAATCTTTTTTAAGACAACAAGCTACTTTAACACCAT
CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTTATCAATCAATTCGGTTAATCCCT
TACTGAGAAATTTCTCAAATTTACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

TATCCCAAGCGCAACCACCAGCACAGTCCCAAACCTCAACAACGGGTACCAGTGGCATAACC
AAAATGCTTCATTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACCT
CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTCTAATTTCTCATATC
AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGCCGACTTGATCT
ATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAACAGGGCTTGAATCGTTCTT
TAAGCGGACTGGATTTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAAINDAQDNNINTETNDQETNQOSIETRDAIDKENGVTETGENSAKNA
EQNVSSTNLNNAPTNGALDDVIPNAIVIKNIPFAIKKEQLLDIIEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTQVITSLNGKEISGRKLKVEYKKMLPQAERERIEREKREKR
GQLEEQRHSSSNLSDLSLSKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS
SNNNNSGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF
NDPDTLEIYSQLLLFKDREKYYYELAYPMGISASHKRIINVLC SYLGLVEVYDPRFIIIR
RKILDHANLQSHLQQQGQMTSAHPLQPNSTGGSMNRSQSYTSLLOAHAAAAANSISNQAV
NNSNSNTINSNNGNGNNVIINNNSASSTPKISSQGQFSMQPTLTSPKMNIIHSSQYNSA
DQPQQPQPQTQQNVQSAAQQQSFRLRQQATLTPSSRIPSGYSANHYQINSVNPLLRNSQI
SPENSQIPINSQTL SQAQPPAQSQQTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSQLLP
QHTNGSVHSNFSYQSYHDESMLS AHNLSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCTTCCACCGTCGGAAGAAACACTT
CTGAAGTGTTAAGGGTAATCGACGCCCTTGCAATTGACTGACAAGGAGGGCGTAGTAACCTC
CAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTCCCTCTGTCTCCAATGATGAGG
CGAAGGCTAAATTTGGTCAATTTAATGAAATTAACCCCTATTTAAGATTCAACCAAGTCGA
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTAACTAAA
ACTTTTATCTATCTTTTATTCTTATATATCTCATCTCGTACGAAGGGCCGCTCATTTGGA
TCATTTTTCTTTACATACCGTAAAGGAATGGCGTTAAAAATATATATATATGAAAATGCA
TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC
TGCGTATACGCATTCTCGTCATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT
TTAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC
CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAATCAACCATAGACCAG
TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAAATTTCC
CTCATCTTGTCTCCAGATGCGAAAAAATTTGGTCTCCACTGTGAAATCAATCCTCAATTCA
GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA
AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCTGTTTCTTTTACAACAGATTCCCA
TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAACCTCCAACCTCCGGGTACTATTA
TCCCTAACCAGATTCTTCTCCTTCTCAGGTTCTCCAACCTTCTTCCGCGGCTCAACGAG
ATTCTAAGGTTTCAGTTCAAACCTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC
AGGGCAGCAATACGAATAAATTTAAAGCAAATAATGAAGCATCTTCTCATATGACGTTGC
GCGCATCTTCTTTAGCGCAAGATTGCAAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC
CCCCGCTGCTAAATGACTCAGCATTGCCTAATAATTCAAAGAATCTTTACCTCCTGCTT
TGCAAATGGCTTTTTATAAGAACAACCTCTGCAGGTAACACTCCGAACGGCCCCCTTCTCTC
CAATTCAAAAAACATATTCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC
AACCACCATTTGCAGCAACAAGCCACGTAGCAACAAATAACAATGCAGATAGGACGAAGA
CGCCGGTAGTAGCCACCACGACTATGCCATTATTGCCTTCGCCGATGCAAAATGTAG
ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACCATA
TTTTCTGTGACTAGGTATCTGCCGATTTTTCTTATTTATGTATTTCAATAACGCCACCGAAT
TATACTCCCAATCTCAGTTGCTTTTCTGGACCGTGATGTTGACGGCATGTCTGTCTGATC
CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT
GCTGGATAAGAACACCTAGATCCACACATATTTTCGCAAGCTTTGTTAATATTGTGCATTT
GGCCTTTGCCTAACCAAAAGTCCTAGATGATTGTTCTTACCGTTTTGTAGGATTAGCAA
AGTCACTGTCTTATCAATTAGGTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA
CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT
TTGCCGCAACTTTGTTGGGCGAGTATCCTTGGTPTTGCCACCAACTTCACAGACAGACTATT
TATTGAAAAAGCCCTTATCCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA
TTGACAATAACAATGATAAAAGGAACAAGAAAGACGAGCCGACGTTGAAAGTAAAT
ACAAACTACCGGGCAGTTTTAGAAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAAATTTGT
CTCATATCATTTGGTTCTTCCACTTCCAGTCTTGATGGTTTTATTGGAACCAAGTATCGTG

CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACCTTTAAATTTCC
AGAGTGACGATACTGTCAACATTTATTTCTTTTATGTTAAATTAAGTGTCTGTTGTTTTG
CATTCCTACCCGAAACACCTCCTACCGATCAAATTCATATGTCACAGAGGCCTATCTAA
CAGCTACTAAAATTGTCACTCTATTGAATAATCTTTTAGAAAACACACCAATTAATTGAAC
TGCCATTTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT
TGACTCCTTTACTTCCTGACAAATATTTTGATTTCAGCAAGGCAATCCGTGGTCACTATCC
ATAGACTTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTTGAGAATGATATTTTCGA
GAACTGCAAGTATGTTAGAAAACTGAACCTTCGTACTGATCATGCATCCAGAAAGTTTTTG
TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG
ATTTGGTTTGGTGTGTTTCACGAGGCGAGAGAAGGGAAATGGATCCCGAATAACAAGC
AAGCCTTAGAGAAAGCCGCTAAGAAAAAGAAATTTTCTCAAATGGTATCTACAATGGCA
CTTCGTCTACGGGTGGCATAACGGACAGAAAACCTATATCCATTGCCACTATATAACCATA
CTTCAGAGATGACTTTGAACTGTAAACAAAACAACACCAAGTGAACCACTGTTACCA
CTTTAGTTCCTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAATAACG
GAGATTCTGACGGTTCTATAATGGAGATTAACGGGATACCTCTTTCCATGCTCGGGGAAA
CAGGCAGCGTAAATTTCAAAGTTTATTCGCTAATACCTCGAATAGTAACGATTATAATA
ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCTCTAATTCATTTATC
CAGTGGCTTCTGTCCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA
GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA
ATCATTTCCTGCGTCCGTTCCAGGGTTAAGGAACCACCCCGTTGGCAACTTATCTAATA
ATGTTACATTGGGAATAGACCACCCTATTCCAAGGGAGCACAGTAATTTACAAAATGTCA
CCATGAATTATAATAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA
TGTCCTCATTCACGTACACCTTTGTTTCGGTCAATATATGACAGTTGGATTCCGCGTCCGA
CCCCGGTCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MVKDNRSDSDQDQDFSSAHMKRQPEQQQLQHQFSPSKQRI SHHDDSHQINHRPVTSCTHC
RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKGSQQLQLLRQDVDEIKSKLDTLLA
NDSVFVHLLQQIPMGNSLLNKLNLHPTPTPGTIIPNPDSSPSSGPTSSAAQRDSKVSQ
TYLSREPQLLQANQGSNTNKFANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLNDS
ALPNNSESLEPPALQMAFYKNSAGNTPNGPFSPIQKTYSPHTTSTTVTTTTNQPPFAAT
SHVATNNNADRTKTPVVAATTTTMTPLLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL
PYFPIMYSNNATELYSQSQLLFWTVMLTACLSDPEPTMYCKLSSLIKQLAIETCWIRTPR
STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN
AEKWRTRTWLGIFFAELCWASILGLPPTSQTDYLLEKALSCGDEESEEDNNDSDNNND
KRNKKDEPHVESKYKLPGSFRLLSLANFQAKLSHIIGSSSTSSPDGLLEPKYRAETLSIL
GKELDLLAKTLNLFQSDDTVNIYFLYVKLTVCCFAFLPETPPTDQIPYVTEAYLTATKI
VTLNLLLETHQLIELPIYIRQAATFSALILFKLQLTPLLDPKYFDSARQSVVTIHRLYRNQ
LTAWATSVENDISRTASMLEKLNFLIMHPEVFVEEDGII SRMRSHLTGSLFYDLVWCVH
EARRREMDPEYNKQALEKAAKKRFSSNGIYNGTSSSTGGITDRKLYPLPLYNHI SRDDFE
TVTKTTPSGTTVTTLVPTKNALKQAEKLAKTNNGSDSGSIMEINGIPLSMLGETGSVKFQ
SLFANTSNSNDYNNNRLLDASNDISIPSNSIYPVASVPASNNNPQSTKVDYYSNGPSVI
PDL SMKRSVSTPVNHFASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNVMTMNNNQ
FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPVL

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGAGTACGAATTAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
ACCCAATTGGTGATGAAGAACAATCTATTAATGACACCATTTTCAAATTTAAAGTGTTCA
AATTATGAAAACAACCTCATATAAATACGTACAAATTTTCTCTACTCGAAGTGATATAGA
TGTATATGTGTAAGTTTACGTTTAAAGTTAGAGTCATGTAATGCTAAGTGTCTCCACCGAT
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGGTT
ATTTTCGGCGGCGGCAAAAATATTTGGTATAATTATGGAAATACAAAAGGGGAACCAT
AAAGGTTGAGGAGGGGATTGATAAGAGAATCTAATAATTGTAAAGTTGAGAAAATCATAA
TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAA
GGAAGGCGGAGTCGGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTTGCG
AAAAAGCTGAAAAGTCAGATATTCAGAGATTGATAAGCGTAAATATCTAGTTCTCTGCTG
ACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAAGAGAATTATGCTACCCCTGAGA
AGGCCATCTTCATTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACAAGGATAAGGACGGGTTTTTGTATGTCACCTTACTCAGGAGAAAATA

CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGLYVTYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)

GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCCTGT
CAAGGTGCATTGTTGGATCGGAATAGTAACCGTCTTTACATGAACATCCACAACCAACGA
AAGTGCTTTTCAAGCATTGCTTGATTCTAGAAAGATCGATGGTTATTCCCTCCCCCTT
ATGCGTCCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTTCGCACTTAGCGTGCTCGCA
ACACAAAATTAAGTAATATGCGAGTTTATAGATGTCCTTGCGGATCTATGCACGTTCTTGA
GTGGTATTTATAACAACGGTCTTTTACCCCTTATTCCTAAACATATAAATAGGACCT
CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTTATTCTACTCTCTTATACTAAT
AAAACCACCGATAAAGATATATCAGATCTCTATTAAAAACAGGTATCCAAAAAAGCAAACA
AACAACTAAACAAATTAACATGTCATTAAACAGTCCATTTTTTGATTCTTTGACAACA
TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG
CACCAAGACGTCAGTTAGCAAACACACCCGCAAGGATTCTACTGGCAAGGAAGTTGCTA
GACCAATAACTATGCTGGCGCTCTTTATGATCCAGAGATGAAACCTTAGATGATTGGT
TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGGTTTCCCTAGAAGTGTCGAGTTC
CAGTTGATATTTGGACCATGACAACACTACGAGTTGAAAGTCGTGGTTCTGGTGTCA
AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCATAATTTGGTTTCTG
GTGAAATTCCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA
GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA
ACATTAAAGCAGACTACGCAAATGGTGTTTGACATTAACAGTTCCAAAATTGAAGCCTC
AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAA

YBR072W, 214 aa (SEQ ID NO 14)

MSFNSPFFDFDINNEVDFAFNRLLEGGLRGYAPRRQLANTPAKDSTGKEVARPNYAG
ALYDPRDETLDWFDNDLSLFP SGFGFPRSVAVPVDILDHNNYELKVVVPGVSKKDDID
IEYHQNKQILVSGEIPSTLNEESKDKVKVKESSSGKFKRVITLPDYPGVDADNIKADYA
NGVLTLTVPKLPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)

AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAAAGTGACCTGGCTCTATAGTGTTGTCCCTCTCGCGAGGACCATTGTTGCTTGCATA
TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA
TATATGAGTTGATGAATAAATAGTTATAAAAACTTGCTTTGGCTTCGATATATGACCGTT
ATTTTTGACTAAGTTTAAACGAAGGAATCTAACCTCGTTCTTGTAAATTACCAAAATCTTC
AACAACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCTA
CTTCTACTTCTGGGAAAGGCATTTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA
AAAAATAAAACCGGAAGAGCTAAAAAAGAAAAACCTACTATAAATAACCGATTAG
AATCGAGTTTTTGTATTGAAATGGCGGTAATAAGCGTTAAACCTCGACGAAGAGAGAAGA
TCCTACAGGAGGTAAAAACAGCTCGGTATATCAAAACGGTATTGTGATTCCGGTACTACTC
AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA
ATAAGTACACACAACCTCAAACCAACCGCCACTGCAGTCACAACAGCCCCTATATCTAAAG
CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTCCGCGGGACCTACTTTAAATCTTGCCA
AGAAGCCGAATAATCTGTCCCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA
AGCCTACTACCAAAAAGCACAAGACTTGAGTGGTGATGGCTACGCTACCTTAAAAGCCA
GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGTCTAC
CAAGTGATTGAGATTCTCTCTTTCGAAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT
TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCACAAA
ACATGGGAAATCCAGCCACCGACCACAAGCACAACAGAAACAGTGCCTTCTACGAAGA
ATGACGGTGGCAAAATACCAATGCCTCTGTCTCAGCTGTTTTCTACTAAACACTGTGAAAA
GATTCAAATCAGTAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACCAGTC
AAAATTCCAAAGCCAAAAAATATTATCCAGTATTTGATGTCAACAAAATCGATAATCCCTA
TAGTAATGAACAAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA
AATTCTTGGCCCTCATCAGAGGGAAGGGGTGAAGTTTATGTATGATTGCTTAATGGGCT
TGGCAAGACCAACTATTGAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG

AAAATGACTCAGATATTAGTGGATGCCTTTTGGCTGATGATATGGGTTTAGGTAAACAC
TAATGAGTATAACTTTGATTTGGACATTAATTAGGCAAACCTCCTTTTGCATCAAAAGTTT
CATGTTCCGCAATCAGGCATACCATTAAGTGGACTTTGTAAGAAGATTTTAGTCGTTTGTG
CCGTTACTTTAATAGGAAATTGGAAAAGAGAATTTGGAAAATGGTTAAATTTGTCAAGAA
TAGGTGTTTTGACATTAAGCTCAAGGAATTCCTCTGATATGGATAAAATGGCTGTCAGAA
ATTTTTTAAAAGTGCAACGAACCTTATCAAGTCTTGATTATTGGCTACGAAAAACTCTTGA
GTGTTTCTGAAGAATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG
GCCATCGACTAAAAAACGGGGCTTCTAAAATTTTAAATACGCTGAAGAGTTTAGACATAA
GAAGGAAGCTTTTGCTTACGGGAACCTCTATACAAAATGATCTTAATGAGTTTTTCACTA
TTATAGATTTTCATAAACCCAGGAATCCTTGGAAGCTTCGCTTCTTTCAAAAGAAGATTCA
TTATCCCTATAACTAGAGCCAGAGACACTGCAAAACAGATACAACGAAGAATTGTTGGA
AGGGGGAAGAAAGGTCAAAAGAGATGATAGAAATTACGAAAAGATTTATTTTGAGACGAA
CAAATGCGATTTTAGAAAAGTACCTTCCTCCAAAGACGGATATAATTTTATTCTGTAAAC
CATACAGCCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG
GACAATTGACGTTTCACTTCTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTA
CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC
AGGACAGCTATAGTCGTTCTTTGAACTCTGGTAAGTTAAAGGTATTAATGACATTACTAG
AAGGTATTAGGAAGGGTACCAAGGAGAAGGTTCGTCGTAGTGTCTAACTACACTCAACAT
TGGATATAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT
CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTCAATCGGAATCCAGCCATAT
TTGGATTCTTGTGAGTGCAAAATCGGGAGGTGATAGGATTGAATCTAGTCGGTCGTTCCG
GACTTATTTTATTGATAATGATTGGAATCCTTCAGTAGATTTGCAAGCGATGTCACGAA
TTCATAGAGATGGTCAAAAAAGCCGTGCTTCATATATAGACTTGTCACAACTGGGTGTA
TCGATGAGAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG
GTGACTCGGAGATGAGAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT
TGAAGGACCTGTTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT
CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG
TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCGCTGGATTTACAAAAGAAAA
TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCTCG
TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATCACAG
ATTCGTTTACCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAGCCCGGCGAGATAT
GTCTCAGAGAACAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQUIPKYENKPFKPRRVGSNKYTQLK
PTATAVTTAPISKAKVTVNLKRSISAGPTLNLAKKPNLSSNENTRYFTIMYRKPTTKH
KTSWSDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSLSLFTLTKAGSNEVQLDYELKE
NAEIRSAKEALSONMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTVKRFSVTK
QTNEHMTTVPKTSQNSKAKKYYPVFDVNKIDNPIMNKNAAA EVDVIVDPLLKGLRPHQ
REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLGKTLMSITLI
WTLIRQTPFASKVSCSQSGIPLTGLCKKILVVCVPTLIGNWKREFGKWLNL SRIGVLTLS
SRNSPDMDKMAVRNFKVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDGHRKNG
ASKILNTLKS LDIRRKL LLLTGTP IQNDLNEFFT I IDFINPGILGSFASFRRF IIPITRA
RDTANRYNEELLEKGEERSKEMIEITKR FILRRTNAILEKYLPPKTDI ILFCPKPYSQQIL
AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGS DPYKSHIKDTQSQDSYSRS
LNSGKLKVLMTLLEGRKGTKEKVVVVSNYTQTLDI IENLMNMAGMSHCRLDGSI PAKQR
DSIVTSFNRNPAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDGQK
KPCFIYRLVTTGCIDEKILQRLMKNSLSQKFLGDSEMRNKESNDDLFNKEDLKDLSV
HTDTKSNTHDLICSDGLGEEIEYPETNQOQNTVELRKRSTTTWT SALDLQKKMNEAATN
DDAKKSQYIRQCLVHYKHIDPARQDEL FDEVITDSFTELKDSITFAFVKPGEICLREQ

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)

AGATCCTAAACAGCACGAAGCATATTATTGCGCATAATTTGTTCTTGTAGGATCTTTTC
TTGACATTTTTTTTCACTCTGCGAGAACTTCTCTTTTTTTTCTCTTCTAGGGACGAAAA
CAAACAAGGGCACTTTTTTTTATCTTTTTTTTTTCTCTGTTGTTTTCAAAACAAAAAGAT
TCCACCACATACATCAGTGTGAAAGACTGTAAAAGCTTTCTGATAAATAAGCACTTTCCAT
ATTTTTCAACTGAAAAATAGTTTTCTTTTGCAGCTATTATTGACTTCATTAAGAAATAT
CCCTTTTTTCCCGTTGCAATTATTTCTATAAGGGAAGCTGGAAATAGGGGGCTGAAAAA
GATATTTGAACAGTCGCTCCAATAACCGTTCTCACCATCATTAACATTTTTTGAAGGTGAA
TACTGTTTCCGTCGATTTATGGCTAATTTGTCAAATACATTTGAAAAAGATTAAAAACAAG

CACAAGCGGTTGAGCATACTATGTGCGCAGACAATTACATCTCTAGATCCGAATTGTGTTA
TTGTATTCAATAAACTTCGAGTGCAAACGAGAAGAGTTTGAATGTGGAATTCAAACGTT
TGAATATACATTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA
GAATCCATCAGGATAATGCGAAACCGCTTTTTCATTTTTGCAGAATCTGGACTTCATTG
AATCCATCATACCATATCATGATACTGAATTGTCCGATGATTTGCATAAACTGATTTCTA
TCAGCAAAATCAAAAATACTGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT
TGACCAATAATCCCAAACAATCCTTATATTTTGCATTCTTACAGAACTATATAAAATGGT
TGATTCCCTTCTCCTTTTTTGGATTATCAATTAGATTTTTATCTAATTTTACGTATGAAT
TCAATTCACATACTCGCTGTTCCGATCCTATGGACATTGTCAATTTACAGCCTTTTGGC
TTTATAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTCTACCA
TTGAGTTTCTTCAAGATAAACAGAAAGCCCAAAAAAAGCTAGTTTCGGTTATCATGTTGA
AGAAATGTTGTTTTATTCTGTGGCTTTGTTGTTTGGCGCAATATTACTATCATTCAGC
TATATTGTTTTCGCTTGAAATTTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA
TCTTGCTTTTTTGCCTACTATACTTATTGTCAGTTTACTCCGGTTTTAACTGTGATTT
ACAACAAAATTTTCGTAGAACCAATGACAAAGTGGGAAAATCATAGCAGTGTGTGAATG
CAAAGAAATCTAAAGAAGCTAAGAATTTGTTATTATTTTTCTATCCAGTTACGTTCCCC
TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTTGTTGACCGCAGAAATAAGAA
CTAAGGTTTTCAATGCCTTTTCAATATTGGCCCGTTTACCTACCCATGATTCAGATTTTA
TTATTGATACAAAGCGCTATGAAGATCAATTTTCTACTTTATTGTTATCAACCACTGA
TTCAATTTAGCATGGAAAATTTGTTCCAAGCCTTGTAGCATTGCTCAGCAGAAAATTA
ATGGACCAAATCCTAACTTTGTCAAAGCTGAGAGTGAATCGGTAAAGCTCAACTCAGCT
CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAACAGACCCCTGGGGAGCAA
CATTTGATTTGGACGCCAACTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGTATGT
TTTCTACAATTTGGCCACTAGCTCCATTTATCTGTTTGATAGTCAATTTGATTGTTTACC
AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT
ACGATAAGCCATCCTCTGTGTCTAATACCCAAAACCTGACGGTTGGTCTATGGAACCTCTG
TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTGACCTATATGTACC
AGAGCTGTAATATACCAGGTGTGCGCGCTCATACTTCCATCCATACGAATAAAGCTTGGT
ACCTAGCAAAATCCAATAAAACCACTCGTGGATAAATATTGTACTATATGCTGTTTATTG
AGCATGTTAGTGTGCTATTTTTCTTCTTTCTCTAGTATTTTGAAATCTTCCCATGTG
ACGTTGCAAATGGCATTGTGCCAAAGCATGTAGTTAACGTGCAAAACCCACCAAAACAAG
AAGTCTTTGAAAAAATTCCCTCCCCTGAATTTAATTCGAATAACGAAAAAGAACTAGTTC
AAAGAAAAGGTCCTGCGAATGAGAAGTGCACCAAGAACTCGGTGAGAAACAGCTGCCT
CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAATGATCCGTCTTCTT
TATCCTCAGCTCCTCGCCTTCATTATCTTCTTCTTCTTAGCAGCAAAACCGGTGTAG
TCAAAGCTTTGATAACGATACAGCCGATCTGCTGGTAAAAGCCATTGGCCACAGAAA
GTACTGAAAAAAGAAATCTTTGGTGAAGGTGCCTACCGTTGGCTCATATGGTGTGCGG
GCGCCACTTTACCAGAAACAATTCCAACATCTAAAAATTACTACTTAAGGTTTGTGAGG
ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCAGAATCTTCCAACGCCACCAATAACA
ACACCTTAGGCACGGAAGTAAGCTTTTGCCAGATGGTGACGCCGTTGATGCACTAAGTA
GAAAAATTGATCAAATACCCAAAATTGCTGTTACTGGTGGCGAAAATAACGAAAAATCCC
AGGCCAAAGACGATGCTGCCACTAAGACTCCACTCATTAAGATGCAAAATATTAAGCCTG
TTGTCAACGCAGCTGTTAACGATAACCAATCGAAGGTTTCAGTGGCTACTGAACAAACAA
AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAACTA
AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACTACAGATGCTACTC
AGCCCCACCATCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA
ACAATTCTAAGACAACCGAATCCTCTTCTCTTCATCGGCGGCAAGGAAAAACCAAAAC
ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)

MSQITISLDPNCVIVFNKTSSANEKSLNVEFKRLNIHSIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDELSDDLHLKLISISKSKILEAPKQYELYNLSNLTNNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSTAFWLYKYEPF
WSDRLSKYSSFSTIEFLQDKQKAQKKASSVIMLKKCCFIPVALLFGAILLSFQLYCFALE
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSVNAKKSKEA
KNFVIIFLSSYVPLLTFLFLYLPMGHLLTAEIRTKVFNAFSILARLPTHDSDFIIDTKRY
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVKSQTDPNWGATFDLDANFKLLLLQFGYLVMFSTIWLAPFICLIVNLIVYQVDLRKA
VLYSKPEYFPFPIYDKPSSVSNTQKLTVGLWNSVLVMSILGCVITATLTMYQSCNIPG
VGAHTSIHTNKAWYLANPINHWINIVLYAVFIEHVSVAIFFLSSILKSSHDDVANGIV

PKHVNVQNPQEVFEKIPSPFNSNNEKELVQRKGSANEKLHQELGEKQPASSANGYE
AHAATHANNDPSSLSSASSPSLSSSSSSSSKTVGVKAVDNDTAGSAGKKPLATESTEKRNS
LVKVPTVGSYGAVAGATLPETIPTSKNYLRFDEDEGKSIRDAKSSAESSNATNNNTLGTES
KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAAVN
DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTDTATQPHHHHH
HHRHRDAGVKNVTNNSKTTESSSSSSSAAKEKPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)

ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC
GTCTATAAACTTCAAACGAAGGTAAAAGGTTTCATAGCGCTTTTTCTTTGTCTGCACAAAG
AAATATATATTAAATTAGCACGTTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAG
TAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG
GCACCTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTCGAAGA
GATCGCACATGCCAAATTATCAAATTGGTCACCTTACTTGGCAAGGCATATACCCATTTG
GGATAAGGGTAAACATCTTTGAATTGTCGAAATGAAACGTATATAAGCGCTGATGTTTTG
CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAACAAATAGAGC
AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT
TGGCCAAATGCAGGTACCATTCCCTTAGGCCAACTAGCCGATGTCGACAAGATTGGTACCC
AAAAAGATATCTTCCCATTTTTGGGTGGTGCCGGACCATACTACTCTTTCCCTGGCGACT
ATGGTATTTCTCGTGATTTGCCTGAAGGTTGTGAAATGAAGCAACTGCAAATGGTTGGTA
GACATCGGTAAAGATACCTACTGTCACTTGGCTAAGACTATCAAGAGTACATGGTATA
AGTTGAGCAATTACACTCGTCAATTCAACGCGTCATTGTCATTCTTGAACGATGATTACG
AGTTTTTCATCCGTGATGACGATGATTGGAAATGGAACCACTTTTGCCAACTCGGACG
ATGTTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTCTTGG
CTCAATACGGTTACATGGTCGAAAACCAACAGTTTCGCCGTTTTTACCTCTAATTCTA
AGAGATGTCATGACACTGCTCAATATTTCAATTGATGGTTTTAGGTGACCAATTCAACATCA
CCTGCGAGCTGTCAGTGAAGCTGAATCCGCTGGTGCCAACTTTGAGTGCTTGTAAC
CATGTCCTGCTTGGGACTACGATGCCAATGATGACATTGTAATGAATACGACACAACCT
ACTTGGATGACATTGCCAAGAGATTGAACAAGGAAACAAGGGTTTGAACCTTGACCTCAA
CTGACGCTAGTACTTTATTCTCGTGGTGTGCATTTGAAGTGAACGCTAAAGGTTACAGTG
ATGTCTGTGATATTTTACCAAGGATGAATTAGTCCATTACTCCTACTACCAAGACTTGC
ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTCGGTTCCAACCTTGT
TCAATGCCTCAGTCAAATTATTAAGCAAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA
GTTTTACCCACGATACCGATATCCTAAACTTTTTGACCACCGCTGGTATAATTGACGACA
AAAACAACCTTAAC TGCCGAATACGTTCCATTATGCGGCAACACTTTCCACAGATCCTGGT
ACGTTCTCAAGGTGCTCGTGTCTACCCGAAAATTCCAATGTTCTAACGACACCTACG
TCAGATACGTCATTAAACGATGCTGTTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT
TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT
TCCTAAAGGTCGTAAACGTCAGCAGCGTCAGTAACCTCTACTGAATTGACCTTCTACTGGG
ACTGGAACACTACTCATTAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)

MFKSVVYSILAASLANAGTIPLGKLADVDKIGTQKDIFFPLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGLSFLNDDYEFFIRDD
DDLEMETTFANSDDVLNPHYTGEMNAKRHARDFLAQGYMVENQTSFAVFTSNKRCHDTA
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSDVCDIFTKDELVHYSYYQDLHTYYHEG
PGYDIKSVGSNLFNASVKLLKQSEIQDQKVWLSFTHD TDILNFLT TAGIIDDKNLTAE
YVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND
FYDYAEKRVAGTDFLKVCNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:
859-1563 (SEQ ID NO 21)

TAACTTCTCAACATAATTATGTAAAAAATTATCTCATTAAGCCAGATAGCAAATATATCA
CATATTGCATTGATTAATTGAGAAAAATATACATGTATCTTTTCAGTTAATTTTATTAA
AAATAAATTATTTCTTACTTTTTTTTCTACAGTTTGCACCATTAACCTCTTTTCTTGCA
TCCATACATTTTGAACCTCCATACATCTTATTTTTTTGCTGTTTTTTTTCAGTGTCTCGG
GCATACAGGCCCGCTTATCTTCATGCCGCCCATCATCTTAGGAAACTCTTTCGGTATGGG
CCAAGGGCAGGCGAAAATCCTATGTGCGTGAGCTGATACAATCTCGGCTGGCTTGGTTT
GTAGGGCACGGTCAATGAATGCCTGATGGGAGAAAAATTCATCTTTATGAAAAGTGATCT

TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTCTAA
TGAATCAGCAGCGCTAACCGGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT
AGTGCACATATAATAAAAATTCTCAAGAACACGTTGTTTAAACGAGATAATTCCCTCTAA
TATACACGTACCGACACTTAGGAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG
GAATTTACGAAAAGGGTTTAGAAAATATCAATGAAAATAAGAAAAACCTGTACGGAAGAA
AGGACAGCAGGGATTGTTGGAATTTGTGATATTGGCTTCGGACAACCTTAACTAACAAA
TGGTATTATTTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAAAGACCTTC
GAAATTGATGATGAACACCGTATTCTGTTTCTTTCGACAAGAGAATCGGTCAAGAAGTC
GATGGTGAAGCCGTTGGTGATGAATTCAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC
GACAAACAAGGTTTCCCAATGAAGCAAGGTGTTTGTGTTGCCAACTAGAATCAAGTTGTTG
TTGACCAAGAACGTTTCTTGTACAGACCAAGACGTGATGGTGAAAGAAAAGAGAAAGTCC
GTCAGAGTGCCATTGTTGGTCCAGATTGCGCTGCTTGGCTTTGGTCATTGTCAAGAAG
GGTGAACAAGAAATGGAAGGTCTAAGTGACACTACTGTTCCAAAGAGATTGGTCCAAAG
AGAGCTAAACAACATCAGAAAGTTCTTCTGCTTGTCCAAAGGAAGATGACGTTCTGATTTT
GTCATCAGAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA
AGATTGGTTACTCCTCAAAGATTGCAAAGAAAAGAGACACCAAGAGCTTTGAAGGTCAGA
AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG
TCTGAAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD LAVLALVIVKKGEQE
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQRKRHRQALKVRNAQAQREAAAEYAQLLAKRLSERKAKEAIEIRKRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTTGTTTGTCTATTCCAACATAATCAATTAGCAGCACATGTGCGACCAACAG
ATAAACACAGCAGCGGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGTGTTTGTGC
AGTGTATTACCAACTTGCGCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCTTT
TAAACCGCTTCCACGGGACATGGGTTCTAATTATGGAGAAGATCAAGCTTTGAAATGGCC
CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGGTTGTC
TATCAGTATATACTCATTTGTGTTTTTCAAAAAATCTCTGGGTGTTTGTAGATGCCACTATA
TTTCTATTGCTATTATTTTTATGTATACTTATTTTGCTTATTTTTCTTATACTCAGGAA
ACGTCATTGGCTTGATATACTCGACGCTTTATTTCTGCAAATTCAGGTCTCAAATCTGAA
CGGCGTGAGGCCACCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCCACATCAAAAAC
ATCATGGCCAATGTCAAATCACTGTACTTCTCCAAACACTGTACGACAAAACAAAACAA
ACAACTCTTGTTAGTAAAAAGAAAGGGAACTAGTAATATGGAGACACATCGTAAAAA
AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCACGGACATG
GCACTAACCACTATGAATACCAACAACAGTATAGCTAAATTTGGACGCGCAGAGAGTTA
GTAGAAGAAGAAGGAAGAAAAGGGAAGCGGAGAGAAGAGATTATGACACATACAACTAC
TCATTACTCTTTGTTCTTTATTATTCTGTTGGACCTTTGTTTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)

MELAKERNGPHQKHGQCQNHCTSPNTVRQNKTNKLLLVKKKGKLVIVRHIVKKMLHIRL
VVLWSHYPEQHGHTNHYEYTNNSIAKLDAQRVSRRRRKKREAERRDYD TYKLLITLCSL
LFVGPLFLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)

ACATGACCTAATTTATAGCTTAGGGTTCTTTTTTGTCAATTCATGCGTATGACAAAAGA
GCACCACGATGGTGATCGAAATCTCTAGGAGTAGCATACCACAGCGATATTATTTAGTAG
TAGGCGGTTTATTATCTTTGTCCCTTTATACTGTTGTGTTTCTTGCTTATTGCTTCAGTA
GGCAGCGTATAGTATAACCAGAAAAAAGTGAAAAATAAACTAAAAAAGCACTATGAGATG
AACGGTAAAAATCCACCAGAGATTTGCTCACTAATAATCCTGTACCATGTCCATCAACCT
ACATTCCGCACCCGAGTATGATCCATCTTATAAGCTGATCCAGTTGACACCAGAGTTACT
GGATATAATACAGGATCCGGTTCAAATACACAGTTAAGGTTTAAAGTCATTGGACAAAAGA
CAAGTCTGAAGTTGTACTGTGTTGTCGACGACAAGACTTGGGTGCTGCAAGCAGCGCAAAC
ATTCAAACACAGTTCTACTAATGAGAGAATTTGTTCTTGAACAACCTATTACTTTTCGACG
AAACGCTCTTGTGTTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTGCCAAGACTG

AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTCAGTACCAATAT
ACAACGGGAACTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCTTGGAAGAACTACTTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAAT
GGCATAAGATTTGGTGGATCTGTGAAAGACGGTGTGTTGTGTATTCTTTCACAAGACTTCC
TTTTCAAAGCACTGCATGTACTACTGATGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAGGACATTGAGGACGAGTCAATC
CATACACAAGAGAAATCATTGAAACAGTGCTGAATAAATTTGCTGTTCAAGAGCAAGAGG
CTGAAAACAATACGTGGCGCTTGAGAATACCGTTTATAGCTCAGTGGTACGGGATTCAAG
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGGA
AGTCCCTTTTCCACCTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCCTGTTTAGGCTACAGTCACAGTGGGACTTGGAGGATATCA
AGCCTCTAATTGAAGAACTAAATTCAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCGCCGTAAAAGACTGGGCAAAAAGACCGTGGTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)

MREFVPEQPITFDETLFLGLSKPYMDVVGFakteSEFETRETHGELNLSVPIYNGELDF
SDKIMKRSSTKVIGTLEELLENSPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAEsLDLQHLNVEDTHHAVGKDIEDEFNPYTREIIETVLNKFVQEQEAEENNTWR
LRIPFIAQWYGIQALRKYVSGISMPIDEFLIKWKSLEFPFFPCDIDIDMLRGYHFKPTDK
TVQYIAKSTLPMDPKERFKVLFRLQSQWLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)

GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAATAAT
GACCTTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC
ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAGGTACATCCGTGCTATGGTCAGAGAG
CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCCGGGGACGAACCAGATTCCAAGAGAAGA
AAATAACGACCCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGACGCTCA
CATGAACACTTCTTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA
TAGACGTTCTTACAAGGTAAAATTTACCCGCGTTTTTAAATAGAATGAAAAAACGTTGT
AGAGTGAAAAGAAAAGCAACAAATATACAGTTTACAAGGCAGCTTCGTATAGTAATACAGC
ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA
CGGATGCTTATATCCCCACGTATCTGCCCCGATGATAAGGTCTCCAATCTGGCAGATTTGA
AAAAATTGATAGAAATGGATTCCAGACTAGATTGTATCTGACAAGAAGGAGGCTGGATA
CGTCCATCAATTTACCTACAAACCAAGCAAGGACCAATCCCCCAATAAAGAGATGC
TGAGGATTTACGTCTACAACACTACGGAAGCAGCCCTCGCAGCGATTCTGGCAGCCCCAG
CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG
CAAACGGAAAGCACCCATTTAGTGAGTTTTTGGAAAGGTGTGCGGGTCGACTTTAAAAGAC
TGAAACCGCTGGGCATGGGCAAGAAGAGGAAACGCGATTTCGTCATTGAGCCTTCCTTTGA
ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG
AGGATGAGGACAGTGCAGAGGCAGAATCCAGGGAGGAAATTGTAGACGCACTGGAATGGA
ACTACGATGAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGG
ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAAAAGTACAGT
ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT
ATTCGATCTACAAGTACATTTTGATCAACAATCTGTTTGTACGGAACAAACAGAGGCTC
AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCTG
GTGACGATGATGGCGTCGAGGGAAGTACTCCAAAGGATAAGCCCGAATTGGGTGAAGTGA
AGCTAGATTCACTCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCCTTGATGA
ATGTTGTGCAAAACCGTGAACAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA
CAATTGATCTTTCCAAGATAACCACCTATGGTGCTACCACCTTGGATGTAGATGTGTCGC
ACATTCTCCACCAGCCTCAACCCAGCCAAATTTACAAAAGAGGAAGAAACAGATGCTG
AAGACACAGCAAACTACGTGAAATCACAAAGCTTGCCTTGCAGTTGAACTCTAGTGCTC
AAAAATACCAGTTTTTCCACGAAGTGTCTTTCATCCAAGAGAAACGCTGACTCACTACT
TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCAGGGCGACCAATACTTCAATGAAGATG
CTGCAAGAACGAGTGACATATACAGTAACAACAATGACAGGTCACCTAATGGGCAATA
TCTCACTACTGTACTCCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28)

MVTQTNPVPVPTYPTDAYIPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRRRLDTSINLPT

NTKTKDHPPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF
SEFLEGVAVDFKRLKPLGMGKKRKRDSLSLPLNLQQPEYNDQDSTMGDNDNGEDED
AESREEIVDALEWNYDENNVVEFDGIDIKRQKDNLRCSITIQLRGVDGGKVQYSPNLAT
LIGMQTGSVNDVYSIYKYILINNLFVTEQTEAQDGSNDAEDSSNENNNKNGAGDDDGVE
GSTPKDKPELGEVKLDSLLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYITIDLSDK
TTYGATTLDDVDVSHILHQPQPQPNLQKEETDAEDTAKLREITKLALQLNSSAQKYQFFH
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)

AGGTTTAAACGCGTTATCTTTGTTCCGAAAAAACGAAAAATATATTTTTTC
GCGTCGCGTTCTCGCGTCTGTTTTGTTTTTCGCGTTCCAATGACCAAAATGGGAAAGTG
GTCGCTTTTGACGAAGGAGACGAAAACCTCTTCTAAAACGTTGGGAGAGAGATAATTACA
TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC
AGCCGCAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTGCGTGCTCTTCCT
CTAACTGTGCACGAGGCACCCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTT
GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGTTTTGCGCCATTTGGCAATTAGCA
ATTTATCAGCATACTTTTCCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTC
TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC
AGAGCTGCTCATTTGGACTTTGCTGCGAGCTTAGACGACTTGTCCTTTTGGGCATCTCTGA
GTTGGATTTCGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTCAGGTCCAGGCT
TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTTGTGAGGTGAGCTTTGCTAGTCTTG
ACGGCTGTAGAGGTGTTTACATTGATGATGAGTCCCTAAGAAAATTTTTCTTTTTTTTC
AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA
TCATCGTCAAAGTTCCTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)

MYLERWWWSCIISQSCSLDFAASLDDLSFWASLSWISKSVRVGLIFSNPSGAGLDLLVFM
RGMSFCEVSFASLDGCRGVYIDDESLRKFFFFFYFTFR CERQMYAFKSQRSIIIVKVPT
TTRVIDLVLVVNVLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)

GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG
CCAGAACTCTCCGCTTCAGCCGCTTTTTGTTGCTGTGTATTTCAGTATATCCATCATCA
TTTTACCTACAAGGAACCTTTTTATAGCCACCCTAAGTAAAACAACATTAGCTTAGC
ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTCTGGCATCGC
TTTTTTACATAAGGTACCAAGGCAAGAGAAAAGACCCGCGAAATTTTCAATTGAGACAT
AGGGTTAAATACGAAATATGTTAAGGTCTAGTTTCCAAAAAATGAAGAAAATGTGATTAGA
CATCCTGGGGAATTAGGTTAAATAGGGCGGGCGCTACAGGGGTTTTCTTAACAAATTT
CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGTAGGTATGGACTAGAACAGAAA
GCAATTTGCAAGCAAGACAATATGACTACGACGGTACCCAAGATATTTCGCGTTTTCAGAGT
TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG
CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCACTGGATATGA
CGAGAGAGGCCTCTTGCAAAGCACAGCATCTGCCGCGGAAGGGAAAAGTGGTAGCAGTG
GTAGTGGCAGTGGTAGCAGTAAGCCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG
GTGGGTGATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG
GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTAACCTTCAGCTCGAATGAAAGCA
ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAATC
CGAAGGTGTACCACATTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT
ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCGTCAAACTTCCGATGTTTCG
ACTTGTTCTGCTTGGTTGTGCCCCGATGGTCATATCGCATCACTCTTCCCTAACTTCC
AGGACAATCTACGTGAGAACTTGCATGGGTGGTGGCCGTGGGAGAACGCTCCTAGTGGGC
CCTCGACCAGAATTTTCGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTTCG
TTGTGCAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAGGCCTGAAAAGG
GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTTCGTGTATCATGGTTTGTGACG
ACGATGCTCTTACGGACGTCCTCGTCACCAAAAAAAGTATAAATTCACCAAGGTTTGT
CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTTPVKIFAFHEFSDVAEAVADHVHQAQDGLAPKNERKHSVPNISMNALDMTREASCK
STASAAEGKSGSSGSGSGSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVRWGDWDIYF
ADERLVPFSSNESNYGCAKRKILDLIDTAKYGTPKVIYHIDESLIDDPQECVDNYEKVLIR
GFAGRDSVKLPMFDLFLGCAPDGHIALSPNFQDNLREKLAWVVPVENAPSGPSTRISL
TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWSFVDDDALTDV
LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTTAATGGCGTAGTTCATCCGCGTTTAATTTAACTA
GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACTGACAGA
CTCAGCTACCGATTAGTGTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTGGACC
TAGTCATCCCTCCACACAAGATTCGCTCTTAAGTAGTGGCGCAGGCTGTTTCGCTTTTAAG
CATAGTGCTTAATGTCTGAAGGCTTTATAGATCCCAAATACTACGCCTTGAGAAATTGAAT
GCACTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGCGCCTGAGGCG
GAGCGTTCGCGAAATCGGGAAAACATTATACTGGGAAAGATCACTATCTATTCTCTAAAT
GAACTTTTAAGCAAATTATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT
AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAAATTTAAGCA
TTACAACGCTATTATTGTTGTTAGTGTTTTTCGTAGCGCAAAATGCGAACTTCTTGACGG
TAGAGATAAAAGAGGAACTTCTAAAGCATTTAGTACTAATATGGACAATATGGCTGGAG
GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG
TAGACGAAGAAATTAATGAAATAAAACAGAAGGTGGGACTCCAACAGCCCATAGCATCGG
TTGATGATAGTTTTGTCGGCCATTAAAAACGATAAAGGGTTCGCGAATAACCAAAGCTTTTA
ATGTTCAAAAAGAATACTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA
GCACCTGTTTCATATAGCAAGGGCATGAAGGAAGTCTTGAAAATGAGTATCAGTTTATCC
CAAACCTACTATATTATAGAACTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA
TCAAGTTGGTGACCGGTAGAGGAACTGTTCCAAACCTTTTGGTTAATGGAGTATCAAGAG
GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAACTTTTAGAATCATTACAAG
TCTGGAGTGATGGTAAATTCTCGGTTGAGCAACGTGAAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34)

MIPSNKRNRILSITLLLLLVFFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA
AMPTSTTNKGSSEVDEEINEIKQKVGLQQPIASVDDSLSAIKNDKGSRTKAFNVQKEYS
LILDLSPIIIFSKSTCSYSKGMKELLENEYQFIPNYIIELDKHGHGEELQEYIKLVTGR
GTVPNLLVNGVSRGGNEEIKKLHTQGKLLESQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAAAATCCAGCTTCTTTTCAAGCAATATTGTCAAAACGATGATGAGAATAGCATTGAAG
AGGATAAGAATTTACGCTATTACAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA
CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG
ATAGTAGCGGCATAGATTTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTA
TCGCGATGTTTGAAAATGGAAAGTAAGGAACGTAATACAAATTGACAAAGTAGCCGACATG
AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATTCATT
GAAGCAATGTGATTCCCTCGATAAGTAAGCTTTTTTCTGTCTGGCGGCGAACCATTAGAG
AACAAAAGACCGAGTTAAGAAAAAGTTTCATAAAAAACTTTTGAAAATGGATGAGTGCTCG
TATAATGGAATAGGAACTTATGCAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC
CAGTAATAATGGCTCGACAACCTCAAAGGAATGCATTATCTGCAGGTCTTGCTTTTGCAG
GTAATGCAACCTCAAATGAGTTTGATGAACATTTGCAAATGAGGTTGAAAGAGAGAGGG
AAATTCAAAGAAAAAATAAAGCGAACTCAATCAAAAAATCGCCAGATTTGATTA
ATAAATCTACTTTTCAATCACGAACGATAGGCAGCAAAAAAGAGAAACATAGACAACCTAG
ATCCAGATCTAGAAATTGTCATCGATGGCCCTCTAAGGAAATCAAGCCCTACCATTTTA
CGTACAGGACCTTTTGCAAAGAGCGTTGGAGAGATAAAAAATGGTTGATGCTTTTATAT
CTGAATTTTCGAGATCGTGAATCTGAATATTATAAAGAACAATCGAAAACGGGGACGTTT
ATATAACGATGAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC
ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTTGAAG
ATGATAACATAATGGTTATTGATAAACCGAGCGGTATACCTGTTTACCCAACTGGCCGAT
ATCGGTTCAATACAATTACGAAAATGCTTCAAATAATCTCGGATTTGTTGTGAACCCAT
GTAAGTAGTTAGATAGGCTTACAAGTGGATTAAATGTTTTTGGCAAAAACTCCGAAGGGAG
CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAAG
TAGTTGGAGAATTTCCAGAAACGGAAGTAATTTGTTGAAAACCTCTAAAACCTGATCGAGC
CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA

CTGTTTTTAAACAGAATCAGCTACGACGGTAAACGAGTATTGTAAAGTGCAAACCGCTTA
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
ATCCTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAGAAAACCTGCTAAAAGTT
GGTTCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTGATCTGTGGTTACATGCCTATC
TATACGAATCAA CTGAGACTGAAGAAGGAACCGAAAAGAAAAAGTGGTGCTACAAAACAG
AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNRLRLNFTVPVIMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKKK
IKRTQSKKSPDLINKSTFQSRITIGSKKEKRLDPEYEIVIDGPLRKIKPYHFTYRTFCCK
ERWRDKKLVDVFISEFRDRESEYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
PPVTSRPIKIVIFEDDNIMVIDKPSGIPVHPTGRYRFNTITKMLQNNLGFVVNPNRDLRL
TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVGEFPETEVIIVEKPLKLIPERLALNA
VCQMDEKGAKHAKTVFNRI SYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
EVWGNLNGKGGQADFDIVITKLDEIGKRKPAKSWFHSNGGYGEVLRQEKCSICESDLYTD
PGPNLDLWLHAYLYESTETEEGTEKKKWYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:
1342-1364 (SEQ ID NO 37)

TATTCGACTAGAAAAAATTAATTTTCTAACTACAAAAAATGCCTGCATATATGTAA
GGATGTAACAGGAAATGTATGGGTCACATATTAATAGCTTGTTTTACTCCATAAAAGAGT
CTGATATTCAGAAAAAACCCCATACATGTTGAAAAATAATGCATTGTGAAAAAAGTGG
TTGAAAAATGTATGCGATCTAGGAAAACTGAATTTTCCTTAGGTTGTGCTCCTCCTCT
AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATCTCTCTGTTTCCCTCTAGCTGAGG
GAAACAGAACTGGTAGCAGTTTCGTTCCGGCCAGGCCGCTGAGCCTATACCACCGAATAT
TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAATGTATA
GGTTACGCAGTAGACTATTTAATATATACCTTTTTATTAGCAGTGTTTCGAAAAATACA
GCAAGAGAATAAGCAACAAGATGTCTGCCGTCCCAAGTGCCAAGTATGTTAAATAATTT
AAACGATGTCACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA
AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTTA
GAACAACGGATCACCATTTACACGTTAAAGACCGAGTAGAAATAACCAATAAATTTGTGT
GGGAAAATATTATACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCTTTGCGGTCTT
ATTTATTCATTCGCTCCCTTGCAATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC
CAGGGTACCTCACTTGTTTACCCCTTTTACACAGTTTACATAATATTTTGGGATTTTGAA
TTTCTGTTTTACTAACATGTGACACGAAATGTTTTTCAATTTTGGTTTTATAACAGACTT
TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCACGTCAGGCGGTAAGGGTTTGATTA
AGGTCACCGGTTCTCCAATCACTTTGGTTGAACAGAAATCCTAAGATTCAGGTCTACG
AACCATTATGTTGGTTGGTTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA
CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG
TCGCTTACCACCAAAGTACGTTGACGAACAATCCAAGAACGAATTGAAGAAGGCCTTCA
CCTCTTACGACAGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAAACCAAAGAAATTCG
GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIAGLVLVYHQKYVDEQSKNELKKAFTSYDRTLIIAD
SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:
709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTTCGGTTAATTTCTCCGCGCTTTCGTTAGACTATTTTGCAAGGACCCAAATAGGAG
ACGCATGGAGGCTTCTACAAAACAGCGTGCCGTTTTGATGGCATGAGCAGGGGGCGCAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTTGGCCACGTAGCCTCAAAGGTTGAATTTGA
CACTTGCTACAGAACTTGAAAAGTACAAAAGGAGGTACATAAAAACAGTAAGCTTGAGA
AGCTTTAAGATATGGTGCAATCGTTACAGAATATTCCTTGAGAAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGTAAATGTGA
TGTGTGTTGCACTGGAAAGCGGAGAACATTATGAAGTAAAGGACAATCAGCACGCCTTC

CAGACTTTTAAGAAACATTGATGGAGCCATTGATATCGGCACCGTACCTAACAAACAACAA
AAATGTCCTGCTCCTGCTACGCTTGATGCTGCCGTGTATTTTTTGCAAGATTATTAAAAGTA
TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG
TACATATACATAAAGCAGAATACTAACAATCGATCCGCTATGCAACAGGCGAAATTCCAT
CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG
AAGGTCATGCTTTAATCATTCCCTAAGTACCATTGGTGCGAAGTTGCATGACATCCCGGACG
AATTCCTTACCGATGCTATGCCGATTGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA
CTTATAATGTGTTGCAGAATAATGGTAAAATTGCGCATCAAGAAGTCGACCACGTCCACT
TCCATTTGATTCTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGCCAGCCCAAG
AAACGGACTTCGATAAGTTGGGCAAGCTACACAAGGAATTGCTTGCCAAACTAGAAGGCT
CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTTTKMSAPATLDAACIFCKIIEKSEIPSFKLIETKYSYAFLDIQPTAEGHA
LII PKYHGAKLHDIPDEFLTDAMPIAKRLAKAMKLDYTNVLQNNKGIAHQEVDHVHFHLI
PKRDEKSLIVGWPAQETDFDKLGLKHLKELLAKLEGSD

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTGGAGACTTTGTGTTGTAGCTTAGAATTTCTTCCACTATATGAAAGCCAAG
ACCTCTTCTCCTCTTTTCGACACTTCGTTTATTTCCACTTTCCCTTATTTAGTATTCATCG
TTCAGAATGCTTTTCTTTATTTACGACGGTTACCACACCCGTACACCTTATCTCATTTC
ACCACTACCTTTTCTTATTAGATTCATCTTATTTTATTTTAGGATTTTGGTTCATTGTA
CGACGCGTGTGCGACCATGGAAAAGGTGTCGCGAGCTGCGATGCTATCCATTTACCCGTCA
TCATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTTATATATATGGAGAGTTA
ACGAATGTAATATTTCTGAATGTTAAATAATTGTTATCCGTCATTATTGTTTCACCTTCTC
TCTTTGAAATTTGCTTGTCTTCTGTTTTCATCTTATATTTTACTTCAATCCTAAGATAG
TCATATCGACTTAATTCCAAATGAGAGCTAAGTGGAGAAAAGAAGAGAACTAGAAGACTTA
AGAGAAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRAKWRKKRTRRLKRKRKVRARSK

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2:
909-1268 (SEQ ID NO 43)

CATGCGGACCTTGTGTGTTTGTCTTAGATTGTTTTATTTTTATGATTGTTGAAGATAT
AAACCACTGTATAGTTGTATAAGATAGGATAATGATGGTGCACTGAAAAATAAAGTTACTA
GCTCTTTAATATTGCAACGGCTTGTAACGGGCGCCATGATGACATTCAGAATTATACCAC
TACTATATGAAAAAATGAAAAGAGGCCCTGCTTTGAACCCGTACATTTTATCTATAATA
TTGCATCTGTGGTTTGCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA
ATTTTCCACCATGGATTTCAGCACCCAAACATTTGAATTTTTTTTCATGTGCGATTGTGAAA
TTTTACTGAAGATGAGGGTAAATAGAGGCCCTGCAATCGTCATCATATGAGAAATGGATAT
ATTGAAAATCTACTCACATCTCTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA
AGAACCATAAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA
TAATGTGCTATGGAAGAAAAAGTCTCCTTTAATGTCTGCAGGATAAAATAATCAAGTGGT
CTGAAGAAAATTTACAGCTACAGTATTACTGCAAACCTTGCAAGGCAAATATCAGAGAGAT
CTCACCAGCTACAACCTGGTAACAGAAATTTATAAGTTTATGGCACTTGTTAAAATTGTT
TGGAAGTTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCATGTGAACATT
TTTTTTGGATAATGCATTGCACAGAGCGTATTAGTGTATACGAGAATCTAAAAATTTGAA
ACTGGCTCATAAAAACAGGAACCTTTACTAACAGTTATGATTTTTTGTTCCTTTCTT
ATCAATAGGCCGGCGTTAAAGCTTACGAACCTAAGAACCAAATCCAAGGAACAATTAGCTT
CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAGTTGTCCAGAC
CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGCTTGACCGTCATCA
ACGAACAACAAAGAGAAGCTGTTAGACAATTATACAAGGGTAAGAAGTACCAACCAAAGG
ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAAATCGAAGCTTCCC
AAGTTACCGAAAAGCAAAGAAAGCAAAATCGCTTTCCACAAAAGAAAGTACGCTATCA
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKEASQVTEKQRKKQIAFPQRKYAIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC
AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA
TGTGGTTAGAACAACATCCAGATGGAGTCACAAATGAATATCAAGGGCCTCGTAGCGATG
ACGAAGACGATGAAGACAGTGAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATAAAGGGTTTTCTTT
AAGTAATGTCATGTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC
GATGCCCAGTGGAAAAGTTTAAAGTGAAAAATTTTTCACACATACAAGTTTAATAAGTT
GGTTTGTATGCAATAGCATTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG
TGATTTTGTATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTGC
CAGATACCCCCAAGGATCAATGTCGCAATTGCGAATATAGCATTTCAAATTGTGAATGCTG
AAACATTAGTATGCCATTATGGGACCAATCTTTTACCGAGCATGAAAGTAAACGGGACGA
CAAAGAGTTTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCATGACGTTATTGGTA
ACGACGACTTTGTTCTTGTTCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC
GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG
ACTTATGGAAGGAATTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA
AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAATGCAGCCAAAATA
CGAAGGATTTGGACGAAATAGTTAGAATAATTGGAAGTTTCAATCCCAACTGAAGAGGCAG
GCTCTGTTCCAGAGATATACTCTCTTTTAAAGGACAACGGATATATTAACAATTGCG
ACAAAAAGTGACTTCCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC
ACACCGATATTAGAGCGTTTTTGCAGAGAAATCTAAGATTTTGTACATGAACAATTTAC
CGCCCGACACAACCTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTAGACCAG
TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCTAACGTTAATAATACTGGA
GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTTGTCTTCC
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC
TGGCAAACACTAAGCAACCAAGGGTGGTGAACATGTCCTTGAGCTTCAACCTTCTTCCA
CCGGAGTACTCGATAAGGCTCAAGAAATTTTATCGCCTTTCCCTCAAAGTAAAAACAAAC
CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACTTTCAAAGACGTACTG
CATGTTTTAGATGTTCTTTTCCGGCACCATCAAATAGTCAAATACATACTGCGAACTCAA
ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAAGTCCGGATCTTCAA
GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGGCCCTGAGTTCAACATGATTG
CTAACCAACGCCAGCAGCTTTAACAATACATAGAGCTATTTTCTGCAATTACGCCAT
TGTCGCGACAAAATTTCATTGAACATGGCACCATCGAACAGTGGGTCGCCGATAATTATAG
CGGATCATTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATTA
ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAAATAACA
TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA
ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA
ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTCCAATATCGGTATGGGAGGAT
GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTCCACGTGCACGTATCATA
ACTTGTCTAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGGCGATG
CAAGTGAACCAATCATTACATAGATTCAACATTGGACCAGCGTCGCGTACTCCCA
GTAATAACAATATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTCCGACCCGATGGGA
ACGATAACAAAGGTCGTGATATTAGTTTGATGGAATTTATGTCACCACCGTTATCGATGG
CAACAAAGTCAATGAAGGAGGGAGATGGGAATGGTAGCTCGTTTAAACGAGTTCAAAAGTG
ACAAAGCTAACGTTAATTTTTCCAATGTTGGTGATAATAGCGCTTTCCGTAATGGTTTTA
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVVLELQVAHLPTPKDQCRIANIAFQIVNAETLVCHYGNSLPSIEVNGTTKSLESA
MVQLDKDIHDTVIGNDDFVLVSLYSTWHIRVTLPRQARDDGFILTSYLQHPKVFDLWKEFD
RWCNVNHPEILGQKKAISNNNCNTKSISINAANKTKDLDEIVRILEVSIPTTEAGSVPEIY
SLLKRTTDILIQLHKKCTSPEDMESVLTKPYDSHTDIRAFLQEKSKILYMNNLPDTTQS
ELESWFTQYGVRPVGFWTVKNIVEDTSNVNNNWSLNNSPYVEDQDSISGFVVFQTHEEAT
EVLALNGRSILSNLANTKQPRVVEHVLELQPSSTGVLDKAQEILSPFPQSKNKPRPGDWN
CPSCGFSNFQRRACFRCSFPAPSNSQIHTANSNNNVNSSRNLLNNRVNSGSSNISNTA
ANHYPGAPEFNMIANNTPAALTYNRAHFPAITPLSRQNSLNMAPSNSGSPILIDHFSGN
NNIAPNYRYNNNNNNNNNNNNNNNNMTNNRYNNNNNNINGNGNGNGNNSNNNNNNHNNHNNHH
NGSINSNSNTNNNNNNNNNGNNSNNCNSNIGMGCGSNMPFRAGDWKCSTCTYHNFKNVV
CLRCGGPKSISGDASETNHYIDSSTFGPASRTPSNNNISVNTNGGSNAGRTDGNNDKGRD

ISLMEFMSPLSMATKSMKEGDGNGSSFNFEKSDKANVNFNVGDNSAFNGFNSSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCCCTTCCGTTGATCTTAGATTTCTTAGAGGTTTCATGAACTAGAAAGCGAC
TTGAACAAAGTCATCCTTCAAGAATCGAAATCTCAAGAGAAAAACAAAATTTAATGTAGA
TTGTCCACTATCTCATGTAAATATACATAACAGGTATTCCCTGAGCGTTCGAAAATTAGAC
TGTAATTTTTCTGATGCGCTCCCGTACACCTTTGACATATACAAACATCCGCACATTTTAT
AGCTTTCTTTCTAGAATTTTTTCCACGCGCTCTCGATCAATGAACTCTTAAAAGTAACTG
ACCCCTAACTTTTTCCAGGCAAGGCTGGCCTCATTACCCTACCCGAAAGTTTCACTTTA
CCCCATGGCAGATGGACGATATTTTAACAAGACGAACTGACCTCGTCTTCTATAAACT
GGACTTCTAAGCAACTCTCATTTATCTTATATCCGTTCCATTTTGTAATAAAGAACCAG
ACCACATCGATTCAATCGAAATGAGAGCCAAGTGGAGAAAGAAGAGAACTAGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRAKWRKKRTRRLKRKRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:
995-1354 (SEQ ID NO 49)

TATTGACGTTTCGCTCTCAGGTCCACCGTGTCTCAAAAGATACTTTTAAAACCTAAAAC
ACACGAAATCATATATTGATAAATCAGAATGATAGTGTGGTACTGTGTCAATTGACTGTT
CAAGACTGAAGAGGATCTTTGATTTGTTGTTACTCAACAAATAATCTTCACGAAAACCTTT
CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTTTAC
ATTTAATTTTTTATCACATAATAGGTAGCTTAAATTGTAAAGTCGCAAAAAAAATGGCA
GCGCAGCCTCTCCGGGTGAACCCACGACAACCTACCTGGCACTCCATGCCTAACGGGC
GGGTTTGGGCAGGATTCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT
GTAATATAATGTTAAGCATACGCTGTCGATTAGCACTATTATTGACCGTAGAATAGGTAC
AGTGAGACAGTATATTGAAATGGTATGTTTGAGATGAACAAATAATAAAGACTGACAA
CTGCAGAACAGAGAGGATCATAGCAACCTAGTAGCAAGAAAGAGCCTCGAAGCGTTAACT
TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG
TAATCAAGTATATCGGATTATTGCAAGCAAAGAATCAAGGAAAAGAAAGTGAAAATAGC
ATACATCTTTAAATTCAGAGGTTTTGCTGAATTTTAATAGGGAAGTTACGTTATGATTG
TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATTCTCCTAATTTTTTTATTGTAAA
AAAGCCTTCCAACGAAATAAATTAGTTATTGGTTTTTTTTCTCTGTTACGAGGGATATAT
GATGCCTGTGCTTGTAGTTCATTATAAGTGCTAATAAAATACTAACGTTAATAAAAATT
TGGAATATTATTTTCATTTTTTATCCTATTAAATAGGCCGGTGTAAAGCTTACGAACTAAG
AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGA
ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG
TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAAGAGAAGCTGTTAGACAATTATA
CAAGGGTAAGAAGTACCAACCAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG
AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGC
TTTCCCAAAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKQYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTTCCTTTAAAGGGATATATAACAGATTCTAAAAGTACAGAAATATTTTCGAGT
GAAGAAGAAGCGTTAAATATTGGATCTTTCCGAGTTCTACTCTGATACATTTTGAAGT
AGGAGAGTCATTTAGAAGGCGTATTGCTCAATAGTAGAAAGCAGGCCTGTGCACATGAAT
TAATTAATAAATATAAAGGTAGTGATTAGACGACACATGTCCATAGGTAACCTGTCATAA
TTTTGAACAATTTCCCTTCTTTTCTTTTTTTTTTTTTGGGTGCGGCATATGTAGCTTGTT
AATTTACACATCATGTACTTTTCTGCATCAAAATATGAAAGGCGATAGTAGCTAAAGAAA
ATACCGAGAATTTCTCGAAAAGTTGACGACAAAAGAAAGGCATAAAAAAGTAATTTGAA
AATATTTTAAAAGTGTTTTAACCCATCTAGCATCCGCGCTAAAAAAGGAAGATACAGGAT
ACAGCGGAAACAACCTTTTAAATGATGGAAACTCCTACAGACAATATAGTTTCCCTTTTC
ACAATTTTGGTAGCTCGACACAATATAGTGGTACCTTGTCGAGAAGTCCCAACCAATAA
TAGAGCTAGAGAAGCCAGTACTCTATCCCCATTGTCAAGAGGAAAAAATGGACGGAAA
AGTTAGCCAGGTTCCAAAGAAGTAGTGCTAAAAAGAAAGATTCTCACCTTCTCCTATTT

CCTCCTCTACATTTTCGTTCTCACCCAAATCTAGGGTCACTTCTTCAAACCTCTTCTGGCA
ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC
ACCCTCACAGAACATCGTCTTTGCCAAGACCTAATCCAATCTCTTTACAGCAAGTAATA
GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAATTTATCAGATAATATACCAC
CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAAAAAATCCTTTTGA
ATGCTTCTTGTACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGAGAGAAAAATTA
TAGAGCTTGCATGTGGCCACTTAAGTCACCAAGAATGTCTTATTATCTCTTTTGGCACCA
CTTCAAAGGCAGACGTTTCGTGCGCTATTTCCCTTTTTGTACCAAATGTAAAAAAGATACTA
ACAAAGCCGTTCAATGCATTCCAGAAAATGATGAATAAAGGATATTCTAATTTCTGATT
TTTTGATTCCATAAGATTCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCCTC
CTTATTCACCACCTCTTGCCTCCTTTTGGGTATCCTATACACCTGTTGAAAAGACAAACGA
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCCAAGGAAA
GAAACCAAATTCACAAAAAAATCAAATATAACATTTTACATTACCCCTGGGGCACA
GAAAGATTCCGTCGGAGCAAACCTCTATCTTAGCAGACACCTCTGTAGCGTTGTACGCTA
ATGATTCTATTTCTGCTGTTTCCAATTCGGTAAGAGCAAAGGATGACGAAACCAAACAA
CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATTCCTTTGAACAATTTCCAGGAAGAAT
TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATTGATGA
TTTCCAAAGATGGTCAGAGATATATACAATGCTGGTGTCTTATTGTAAGACGCATTTG
TAATAGCAGAAGTGGATAACGATGTTGATGTTTTGGAAATTAGACTAAAGAATTTAGAAG
TATTTACACCTATTGCCAATTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA
CCTTAAATAAACAAACATTGCGCCGATTTTACAGATCTTTACATTGTTTCAAGATATAAAT
CTGACGAAAGCACAACCTGTACAGAAAATGGATATCAGGTATATTGAATCAGGATTTTGTAT
TCAATGAGGACAATATCACTTCGACCCTGCCTATTCTTCCCATTATAAAGAACCTTTCAA
AAGATGTTGGTAATGGTAGGCACGAGACGAGTACCTTTCTAGGTTAATCAATCCTAACA
AAGTTGTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA
CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTGACAGTATACAATCTGTTCTAA
CCACGATAAGCTCAATTCTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT
TACAGATCGATTTTACGAAATTGAAGGAAGAAGACAGTTTAATTGTTGTTATAACAGTC
TAAAAAGCTTTAACCATTAAATTTGCGCGTTTGCAGTTTTGTTTCGTTGATCGAAATAATT
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC
TCAAATCAAAGAGTTCTCGACACAATTTTACCTATTTGGTTGAAAAATACTCTATATC
CCGAAAAATATTCATGAACATTTGGGTATTGTTGCTGTATCAAATAGTAATATGGAAGCAA
AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTTGGAAGAAGAAGGCCCA
ATGAATTGAAGATTAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTTGATGAAC
TAGTCGAGGCAGCTCCTGGACTTTTGTTTTAGAAACTCTTTGCTACAGTTTCGGTCTAA
GTTTTGATGAACATGATGACGATGACGAAGAGGATAATGATGATTTCGACCGATAATGAAC
TTGATAATAGTTTCAGGATCACTGTGCGATGCTGAATCTACAACACTATTTCATATTGATT
CTCCATTTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG
AGGGTGAACATAGCAATATAGAAAACCTTAGAACTGTGCTTCTTCAGTACAGCCAGCTC
TGATTCTAATATTAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAATGAAA
ATGAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA
CCAGACGCAGTTCAATTCTCGAGTCTTATAGAGAGCGGTAATAACAACCTGTCCCCTCCATA
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTLSRTPNQIIIELEKPSTLSPLSRGKKWTEKLARFQR
SSAKKKRFSPPISSTFSFSPKSRVTSSNSSGNEDGNLMNTPSTVSTDYLPQHPHRTSS
LPRPNSNLFHASNSNLSRANEPRAENLSDNIPPKVAPFGYPIQRTSIKKSFNLNASC TLC
DEPISNRRKGEKIIELACGHLHQECLIIISFGTTSKADVRALFPFCTKCKKDTNKAVQCI
PENDELKDILISDFLIHKIPDSELSITPQSRFPYPSPLLPPFGLSYTPVERQTIYSQAPS
LNPNLILAAPPKERNQIPQKKSNTFLHSPGLGHRRIIPSGANSILADTSVALSANDSISAV
SNSVRAKDDETKTTLPLLSYFIQILLNNFQEELQDWRIDGDYGLRLVDKLMISKDGQR
YIQWCWFLFEDAFVIAEVDNDVDVLEIRLKNLEVFTPIANLRMTTLEASVLKCTLNKQHC
ADLSLDLYIVQININDESTTVQKWSGILNQDFVFNEDNITSTLPILPIIKNFSKDVGNR
HETSTFLGLINPNKVVEVGNVHNDTVIIRRGFTLNSGECRSRQSTVDSIQSVLTTISSIL
SLKREKPDNLAIILQIDFTKLKEEDSLIVVNSLKAITIKFARLQFCFVDRNNYVLDYGS
VLHKIDSLDSISNLKSKSSSTQFSPIWLKNLTYPENIHEHLGIVAVSNSNMEAKKSILFQ
DYRCFTSFGRRRPNELKIKVGYLNVDSKIDELVEASSWTFVLETLCYSFGLSFDEHDD
DDEEDNDDSTDNELDNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI
ENLETVASSVQPALIPNIRFSLHSEEEGTNENENENDMPVLLLSMDMDKIDGITRRSSFS

SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA
GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCCTACACATATCTCTCTTC
AAGATTATCGTGATGCTAATGCTAGAAGTAATATATCGCGTCAGGACTCTGTCTCCACAA
CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGCGTGTGGCAAACC
CTGATTTCAGACCCAGAATGATATCCTTCTCTGTAGTTTTGTAGATGTCATATATGTACGT
TTATGGAACAGCATTTTAGAAAAGTATTACCCAGCTTATCACTTCGTTTTTTTTTTCTTT
CCGTGTACTCGCTACACGTAGAAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG
ACGTTTCATTAAGACTCAGTTAAGATTGCCTTGAGAATAAAACAAAAGTAATCACAGTTAAC
TATTGAACAAGAGTGCACCTATGACTTCACCTTCTTTCACAGCCAGCGTACACGTTGGTTT
TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTTCAGAAAAGCTCTTGAAA
AGGGATCTGATGAACAAAAAATTGACACGATGAAATCAATTTTAGTTACAATGCTGGAAAG
GAAATCCAATGCCTGAATTGTTGATGCACATAATAAGATTTGTCATGCCCTTCTAAAAATA
AGGAATTA AAAAAGCTTTTGTACTTCTACTGGGAAATTGTTCCCAAAGTAGCTGAAGATG
GAAAATTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTGCAACATC
CTAATGAATATATTAGAGGTAACACATTAAGGTTTTTAACGAAATTGAGAGAGGCCGAAC
TCTTAGAACAGATGGTTCCCTCTGCTTAGCGTGCTTGGAATACCGTCATGCATATGTTTC
GTAAGTAGCAATCCTAGCAGTTTTCTCCATTTTCAAGGTCAGCGAACATTTACTTCCCG
ATGCTAAAGAAATCATCAATTCGTTCTAGTAGCTGAAACTGATCCAATATGCTAAAAAGAA
ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAATGCCTTACACTATTTAGAGAACA
ATATTGCTGATATAGAAAACCTAGACCCTTTATTACAAGCTGTCTTGTTCATTTATCA
GACAAGATGCAACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTGATGGAAC
TGCTTTTCGACCACGACTTCCGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT
TGCTTGCCAATCCAAATGTCTTGGTTCCTGCGGTAAACAAATTGATTGACTTGGCCGTCA
AGGTTTCTGATAATAACATTAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA
ATAACGTAGGTGCTTTGGAAGAGTTAACCTGGATATTTTGAGAGTCTTGAATGCGAAG
ATTTAGACGTTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG
CTGAAGATGTTGTTTCAGCTTTTGAAGAAAGAGCTGCAACAACCGTAAATAACCCAGATC
AAGACAAGGCAATGCAGTACAGACAATTGTTAATAAAAACTATTTCGTACCGTGGCTGTAA
ACTTTGTAGAAATGGCAGCAAGTGTGTTTCGCTATTATTAGATTTTCATCGGTGATTTAA
ACTCGGTTGCCGCCAGTGGTATCATTGCCCTTATCAAAGAAGTGATCGAAAAATACCCAC
AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA
AAGCTTACCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAATAC
AACATTGTTGGAAGCACATTCGTAACAGCGTAGGTGAAGTTCTATCCTTCAATCAGAAA
TCAAAAAGTTAACACAAAACCAAGAACACACCGAAGAAAATGAGGTTGACGCTACCGCCA
AGCCAAGTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTCGATG
TGAAGACTTCTCAAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTCGCC
GGTTTGTTTAAGTGGTGATTCTTACACAGCTGCCATTCTGGCCAACACCATCATTA AAC
TGTTTTAA AATTCGAAAACGTTTCCAAGAACAAAAGTGTATCAATGCTCTAAAGGCGG
AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGGAGAAAA
AAATTGATGAAGATTCTTTAGAGAGAGTTATGACATCTATTTCTATTTTATTGGATGAAG
TTAATCCTGAGGAAAAGAAGGAAGAAGTTAACTTCTGGAGGTTGCATTCCTGGACACCA
CCAAATCCTCATTCAAGAGACAAATTGAAATTGCAAAGAAGAACAAGCATAAGAGAGCAT
TAAAAGACAGTTGCAAAAACATCGAACC AATTGATACGCCGATTTCTTTTCAGGCAATTTG
CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACCTGGCAA
TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTGGAAGCTGAAGAAGATAG
TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGTATTACAAACAATCAAT
TTGACGTCGTATTAGATGTTCTTCTGTTAATCAAACGAAAGAAAACATTGAAAAACCTAC
ATGTGCAATTTGCAACTCTTGGTGATTTGAAGATTATTGACACACCACAGAAGACCAACG
TGATTCTTCATGGCTTCCACAAATTCACGTGTTACTGTCAAAGTTTCTCTGCTGACACAG
GTGTCATTTTCGGTAATATTATTTATGATGGTGCGCATGGTGAAGATGCTCGTTATGTTA
TTTTAAACGACGTTTCATGTTGACATTATGGATTATATCAAACACAGCCACTGCTGACGATG
AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAAACAAAATATCGGTCAAATCAC
AACTACCAACATTGCATGCTTATTGAGAGAACTGGTCAAGGGAACATAATATGGGTATTTC
TAACACCATCAGAGTCGTTGGGAGAAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG
CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCAACCTGTGTATCGAAAAGGATTTCAAAA
CCAATGATGTCATAGGTTATGTTTCGTATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC
TAGGTGACAGAGTGGCATTGATTGCTAAGAAGACCAATAAACTTGCTCTCACTCATGTTT

GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFDPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPEL
LMHIIRFVMPSPKNKELKKLLYFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG
NTRLRFLTKLREAELLEQMVPVSVLACLEYRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN
SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT
PALKAQYIELLMELLSTTTSDDEVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSDDNI
KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL
LKKELQTTVNNPDQDKAMQYRQLLIKTI RTVAVNFVEMAASVVSLLLDFIGDLNSVAASG
IIAFI KEVIEKYPQLRANILENMVQTL DKVRS AKAYRGALWIMGEYAEGESEIQHCWKHI
RNSVGEVPILQSEIKKLTQNOEHTEENEVDATAKPTGPVILPDGTYATESAFDVKTSQKS
VTDEERDSRPPIRRFVLSGDFYTAAILANTI I KLVLFENVSKNKTVINALKAEALLILV
SIVRVGQSSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLLLEVAFLDTTKSSFKR
QIEIAKKNKHKRALKDCKNIEPIDTPI SFRQFAGVDSTNVQKDSIEEDLQLAMKGDH
ATSSSSISKKKIVPLCGFSDPVYAEACITNNQFDVLDVLLVNQTKETLKNLHVQFATL
GDLKIIDTPQKTNVIPHGFKFTVTVKVSSADTGVIFGNIIYDGAHGEDARYVILNDVHV
DIMDYIKPATADDEHFRTMWNAFEWENKISVKSQLP TLHAYLRELVKGTNMGILTPSESL
GEDDCRFLSCLNYAKSSFGEDALANLCIEKDSKTNVDVIGYVRIRSKGQGLALS LGDRVAL
IAKKTNKLALTHV

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)

AAACTTTGTTCAAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACTTATTTTT
ACTGCATGTGGATAAAAGTTTTTCGAATCGTTTGCAGGCAAATGTAACTATTACTTTTT
AATGATTTCTGATACTCTTTGATTCCATTCGTGCATACCTTTTTTCTGCATTGAAACGCT
AATTAAGTATTTCTTGCCCTGCTTCTTTTCCTTTTGATTTCTTTTTTTATCTCAAGTT
TTTAATTTCTGGAGAATCTCTTTTTTTGTTTATTTTGTTAACACAGTTAGTGGAGCCTTG
TAGTATCGAGAGTAGACTATCTTTGGAAGCAATGCGAGTTGAGAGATTGTGGAGTGTCAC
TACAGAACCAATATTAAACACAATCTTTCCCTCAAACGTGTAACACCGAGTTTTTTCGCCA
CCAATCGTGAATCCGATAGCATATACTTTTGTCTAGAAATTTCAATAAAACAACAGAATAA
CGAAGAGTGCTAAGGGACAAATGCAAAACCCTCCGTTGATTCTGTCCTCCGATATGTATAATC
AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT
CTCCGCAAATTGCACAGCCCAGCACGTCCCAAAAGTTACCTTATAGAATAAATCCTACAA
CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA
ACTTGATGCATCTATCTGGTCCGTCTGACTATAGATCGATGCATCAAAGTCCTATACATC
CATCTTATATCATCCCTCCGCAATCAATGAAAGAAAACAATCAGCTTCTTACACAGAC
CTCAAAATGCTCATGTTAGTATTCAACCTTCCGTGGTATTCCCCCCTAAAAAGTTATTCCA
TATCTTATGCACCTTATCAAATAAATCCCCCTTTACCAAATGGACTTCCGAACCAGAGCA
TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA
CCAGTGTTACTACTGCACCTCCTTCTTTTCAAACAGTGCTGATACCGCTAAAAATTTCAG
CTGATAATAATGATAATAATGATAATGTAACCAAACCTGTTCTTGATAAAGACACCCAAC
TCATAAGTAGTTTCAGGCAAACTTTAAGAAATAC TAGAAGAGCTGCTCAAAATAGAACCG
CTCAAAAGGCATTTAGACAAAGGAAAGAAAAATACATCAAGAATCTCGAACAAAAATCAA
AGATATTTGACGATTTACTAGCAGAAAAATAA TAAC TTCAAATCATTAACGATTCATTAA
GAAATGACAACAACATTTTAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT
TAAGAAGTGAGTATGATGTCTTATGTAACGAAACAACATGTTGAAGAATGAGAATAGTA
TAATAAAAAATGAACACAACATGTCAAGAAATGAAATGAAACCTAAAACTTGAGAATA
AACGCTTCCACGCTGAATATATACGAATGATCGAGGATATTGAAAATACTAAAAGAAAGG
AACAAGAACAACGAGATGAAATAGAGCAACTAAAAAAAATAAGATCCCTGGAGGAA
TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)

MQNPLIRPDMYNQSSSMATYNASEKNLNEHPS PQIAQPSTSQKL PYRINPTTTNGDTD
ISVNSNPIQPPLPNLMHLSGPSDYRSMHQSP IHP SYII PPHSNERKQSASYNRPQNAHVS
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQSI SLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKVPDKDTQLISSGKTLRNTRRAAQNRTAQKAFRQ
RKEYIKNLEQKSKIFDDLLAENNNFKSLNDSL RNDNNILIAQHEAIRNAITMLRSEYDV
LCNENNM LKNENSI I KNEHNMSR NENENL KLENKRFHAEYIRMIEDIENTKRKEQEQRDE
IEQLKKKIRSLEEIVGRHSDSAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)

CCGACAGTACGACTTAAAAAACAAAAACAACGTCCAGGTGGAAAAAGCTGCCGCAAATGG
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT
AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG
TTTCTACAAGTATTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT
TAAATCTACACAGTTGCCATATCGTTTATCGCCTTATTCTTCAGAAACATTTTCATCAACTA
CTCTGGTGCATTAATTTTCATGTTAGTTACCATATATACCGGCCGGCCGCATCGGGGTTTTT
TGATTGAAAAAATTGGTATATTTTCAGTACACATATAAATAAAACCCCTCAATTTGCCTCT
CCAACCGTTATAACTATTCCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG
GGATTTTTCATCTAATACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT
GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCAGTTTATGATTC
TAACCATCAACGAATTAATAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA
ACATTTGAAGGATTATTTGTTGTGATCTTTTGTTACAAGCTAATAAGTAATTTTTTTT
ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATATGTTCCA
GAAGATTGTTTCGTTGGTTATTGGACTCACCATTTTGGAGGGGTACCGTAGAAAAGGAAG
TCACAAAGGTCAAACAATCGATCGAAGACGAACTAATTAGATCGGACTCTCAGTTAATGA
ATTTCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA
AATTGAACGACTTGATAACCATACCCAATGGAAGGAAGGAAAGGTCTCTGGTGCCGTTT
ACCACGGTGGTGATGATTTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG
CCAATCAATTACATCCCGATGTCTTTCCTGCCGTACGTAAAATGGAATCCGAAGTGGTTT
CTATGGTTTAAAGAATGTTTAAAGCCCTTCTGATACAGGTTGTGGTACCACAACCTTCAG
GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC
GTGGAATCACCGAACCAGAAATAATTGCTCCCGTAACTGCACATGCTGGGTTTGACAAAG
CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG
TGGACCTGGGAAAAGTGAAAAAATTCATCAATAAGAACACAATTTTACTGTCGGTTCCG
CTCCAAACTTTCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAAAAATAGCACAAA
AATATAAACTTCCTTTACACGTCGACAGTTGTCTAGGTTCCCTTTATTGTTTCATTTATGG
AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA
TATCATGTGACACTCATAAATATGGATTGACACCAAAAAGGCTCGTCAGTTATAATGTATA
GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT
ATGGCTCTCCTACATTAGCAGGGTCCAGGCCTGGTGTCTATTGTCTGAGGTTGTTGGGCCA
CTATGGTCAACATGGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG
CAATGAAGTTTAAAAAATACATCCAGGAAAAACATTCAGACCTGAATATAATGGGCAACC
CTAGATATTCAAGTCATTTTCATTTCTTCAAAGACCTTGAACATACACGAACATATCTGACA
GGTTGTCCAAAGAAAGGCTGGCATTTCAATGCCCTACAAAAGCCGGTTGCACTACACATGG
CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG
TGCAAGAGTTGAAGAGCGAATCAAATTTCAAACCATCCCCAGACGGAACAGCGCTCTAT
ATGGTGTGCCCGGGAGCGTTAAAACTGCTGGCGTTGCAGACAAATTGATTGTGGGATTCC
TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPIHLLREEGDFAQFMILTINELKIAIHGYLRNTPWYNMLKDYL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVKEVTKVKQS
IEDELIRSDSQLMNFPLPSNGIPQDDVIEELNKLNDLIPHTQWKEGKVSGAVYHGGDDL
IHLQTIAYEKYCVANQLHPDVFPVVRKMESEVSMVLRMFNAPSDTGCGTTSSGGTESLL
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPHGIADDIEGLGKIAQKYKLPLHVDSCLGFSFIVSFMEKAGYKN
LPLLDLFRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPATWGGLYGSPTLA
GSRPGAIVVGWATMVNMGENGYIESCQEIIVGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNHELSDRLSKKGWHFNALQKPVLAHMAFTRLASHVVDIEICDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTTGTCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCTGTGGAGCAGAT
TCCTGTGGAACTTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGTCTGT
TCTTCGACTGGGGCATCGACAACAGATTTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT
TCAGACATTATCCTTATGGTTTACGCTAATTGCTTAATTTTGATTCCCTCAAAGTATA
TATATTTAGAAGAGAGGAAATTATTTTCTCATGTCTTTTTTAAATCCCTTTGGGTGGCG
AAAAAAAAGAAATGTAAAAAATTTTGCCTTCGTTTACAGTGATAAATATACGGAGGGGCT
CTATGATAAAGGTAGTAGTAAATCATGAATTGTTGAACAAGCATTGACAGATATGATAA

CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAAGTTACTA
TAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTGCGTCCTCGTATGCCCAAG
CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATCCATGGTTATGAAGTGAGAAGAA
TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCCTCCAGACAGGAG
CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTGAGCATTGCTTTTAAAA
CCAACCTCCAGATTCCACTGGGGTCCCTCATATTCTAGAGCATACAACGTTGTGTGGGT
CTGTTAAATATCCAGTTAGGGACCTTTTTCAAAATGCTAAATAAATCTCTAGCTAATT
TCATGAACGCTATGACAGGTCCAGATTATACATTTTTTCCCTTTTCCACTACGAACCTTC
AAGATTTGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC
AAGAAGATTTTGATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCGGAGA
GTAAATTTGTTTTCAAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAAATGCCA
ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG
GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA
ATTACCATCCCTCAATGCAAAAACTTTCACGTACGGTAACCTTGCCTTTGGTGATACGT
TAAAGCAATTAAATGAGCAGTTCACTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT
TAATGCCTATTGATTTAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA
TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTTGTGGAGCGCCACAGG
ACACATATGATACCTTTTTGTTAAAAAGTACTGGGGAATTTATTAATGGATGGCCATTCCT
CTGTAATGTATCAAAAATTAATAGAATCAGGAATTGGTTTGGAGTTCTCCGTAAATTCAG
GTGTTGAACCACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGGCGTGAGTGATA
TTGAAATATTTAAAGACACTGTAAATAATTTTTCAAACCTGTTGGAACAGAACATC
CTTTTGACCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTAAGAAGGATC
AAAAGGCTGACTTTGGACTTCAATTACTCTATTTCTATACTACCTGGTTGGACAAAACAAA
TCGATCCTTTTGAGAGCTTGTGTTTGAGGACGTTTTCGAAAGATTTAGAGGTGACTTAG
AAACGAAAGGTGATACTTTATTCCAAGATTTAATCCGTAAATATATCGTTTCATAAACCTT
GTTTCACGTTTTCATTTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC
AAACAAGACTGAGAGAAAAAATTACTGCCTTGGATGAACAAGACAAGAAAAACATCTTTA
AACGTGGTATACCTGTTACAGGAGAAACAAAATGAAAAAGAAGATTTATCCTGTTTACCTA
CCTTACAAATAAAAGACATCCCAAGAGCTGGTGATAAATATTCAATCGAACAGAAATA
ATACAATGCTTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC
TAAATGACATAATAACCTTTGAACTCTTCCCATACCTTACCTTTATTTGCTGAATCGTTAA
CTAACCTAGGGACAACAACAGAATCCTTCAGTGAAATAGAAGATCAGATAAAATTACATA
CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCCTAACACCACAGAGCCTCGCC
TGATTTTCGGGTTTGACGGATGGTCTTTAAATTCGAAGACCGACCACATTTTGAATTC
GGTCTAAGATCTTACTAGAACTGATTTCCATAAAAAACAGCGATAAATTGAAAGTCTCTA
TCCGCTTAAATAGCATCTTCAAACACAGCTTGTGTAGCAGATGCCGGTCATGCTGCAA
GGGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCTCAATGGTA
TTGAGCAACTACAATTTATAAATAGATTGCACAGCTTGTAGACAATGAAGAACTTTCC
AAAGAGAAGTTGTGCAAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA
TGAATTTTATACCTCAGACTCTGATGTTCAAGCGAAAACAGTAGAAAGCCAAATTT
CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG
ATTATCCTCTTATTGGATCCAAATGTAAACATACCTTTGATAAAATTTCTTTCCAGGTCC
ATTACACATCCCAAGCTTTATTGGGTGTGCGGTATACACATAAGGATGGCTCTGCCTTC
AAGTTATGTCAAATATGCTAACATTCAAACATTTGCACAGAGAAGTCAGAGAAAAAGGTG
GTGCTTATGGTGGTGGTGTCTTATAGCGCTTAGCGGGTATTTTTCAGTTTCTATTCCT
ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC
TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC
AAGTAGACGCACCTAAAAGTCCCAAGGAGAAGGCGTGACGTATTTTCATGAGCGGTGTTA
CAGACGATATGAAACAAGCAAGAAGGGAACAACTCTTAGACGTATCTCTCTGACGTTTC
ATAGAGTCGCGGAAAAATATCTACTAAACAAGGAGGTGAGTACGGTACCTTGACCTG
GAATCGAGGGGAAGACTGTTTACCAAAATTGGGAGGTGAAGGAAGTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQAVRKYPVGGIFHGYEVRRLPVPELRLTAVDLVHSQTGAEHLHID
RDDKNNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSANFMNAMTG
PDYTFEFPFSTTNPQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG
VVYNEMKGQISNANYFWSKFQSQSIYPSLNNSGDPMKITDLRYGDLDFHHKNYHPSNA
KTFTYGNLPLVDTLKQLNEQFSQSGYGRARKDKLLMPIDLKKDIDVKLLGQIDTMLPEKQ
TKASMTWICGAPQDTYDTFLKVLGNLLMDGHSSVMYQKLIESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIEQLELSKKDQKADFGL

QLLYSILPGWTKIDPFESLLFEDVLQRFRGDLETKGDTLFDLIRKYIVHKPCFTFSIQ
GSEEFKSLDDEEQTRLREKITALDEQDKKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI
PRAGDKYSIEQKNNMTSRITDTNGITYVRGRLLNDIIPFELFPYLPFAESLTNLGTTT
ESFSEIEDQIKLHTGGISTHVEVTSDPNTEPRLIFGFDGWSLNSKTDHIFEFWSKILLE
TDFHKNSDKLVLRLLASSNTSSVADAGHAFARGYSAHYRSSGAINETLNGIEQLQFI
NRLHSLLDNEETFQREVVDKLTQLKYIVDTNNMNFITSDSDVQAKTVESQISKFMERL
PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVYPYTHKDGSAQVMSNML
TFKHLHREVREKGGAYGGGASYSALAGIFSFYSYRDPQPLKSLETFKNSGRYILNDAKWG
VTDLDEAKLTIFQQVDAPKSPKGEGVTYFMSGVTDDMKQARREQLLDVSLLDVHRVAEKY
LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEQ ID NO 61)

CTTTTCTCAGCACCTGTCCAGAGACATAACATCACAATCACATCGCCCCAGTAAATGCA
TACGCAAGATAAGATACAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT
GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA
TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCTT
GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT
GAGGCTGTAATGCTTACCGTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCATACAC
ATTTTTCGGTAACTGCGGCATATAGATGAAAGTTGAAATGAATATTTCAAAAAGAATATATA
TAATAATGCAGGAGATCAAGGAAGAAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA
AATAAAAAGTAAGCAGGAGAATGAATCGTGTGGTATAGACGTAGATCATATGATAGGGG
TCTGCTTCTGGCCGTAGTGGTGGTGTTTTGGGTTGGCGCTTCGTGTTTGACTAATGAAT
TGCTCGAGACAAACGCGTACAATAAACCTTTCTTCCTTACTTATCTAAACATATCATCGT
TTGCTCTTTATTTGACGCCAGATCTATGGAGGATAATCCAATCAAGAAGGAAGAGCTTGC
AGGAACGGACAGAACGAACATTACCTATTCACACACAAGAATCTTTTTCAGAGTTCCTAC
CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG
TGAAGGATACAATGAGGTTGAGTCTGCTATTTTGGCTCTTGTGGTTCTGGCAAATTTGG
CGGCTAACGCTGCTTTGTCTGATACACAGTGGCTTCGTCAACAATCTTTCATCGACAT
CCTCATTTTTTACCTTATTTCTTGCCACTAGTCTAGGAATAGAAACTTTTTCGACAAAAA
AACTGCTGGGGTTATTTGTGTCTTTGTTTGAATTATCTTAATTGTGATGCAATCCTCGA
AGCAACAGGATTCTGTGAGTGCTTCTCCTTTTTTGGTAGGTAACACTTTAGCACTGCTGG
GGTCATTTGGGTTACAGTGTCTATACAACCTTTTTGAAATACGAAATATCATCCAAAGGTC
TCAGACTAGACATTCAGATGTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT
GGCCAATTTTAATAATCCTGGATATAACACATATGGAACTTTTGAACCTACCAAGTAAT
TCCACATTTCTTTTCTTGTGATGTTAAATTGTATCATTATCTTTGTAGTACTATTTT
GGTGATAAGCCCTCATTTTGACATCACCTTTGGTGGTTACCGTTGCCTTAATTTACTA
TCCCGTTAGCCATGTTGCTGATTTTGTATGGCGAGAGGCATTTTTTACGCCTTGGTATA
TCATTTGGTGTTATTTTTCATTTTGTTCATTTCTTTCTAGTTAACCATCGGGGAGAATCTG
CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIDVDHMGVLLAVVVVFWVGASCLTNELLETNAYNKPFFLTLYLNISSFALYLTP
DLWRIQSRRLSLQERTERTLPIHTQESFSEFLPLLSSTPSTSSNLSSIADTKVKDTMRL
SLLFCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFSTKLLGLFV
SLFGIILIVMQSSKQDSVSASSFLVGNLALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTFLFWPILIIILDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALTFTIPLAMFADFVWREAFFTPWYIIIGVIFIFVSFFLVNHRGESAVEKDCA
AVEKGPILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2:
983-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAATTGAGAACGATATTATTAATTCTAGTATATTTTAGGAACAGCA
GGCATTATATCCAAAACCTTTTTTAAAATAGCATCCACATCACTTACTGGCGTACAGTTT
CGTGCTGGCAACAAAAAGTACATTTAATTTCAATGATTAAAAAGACATTAAACATCCG
TACATTACGCACCCATGCATGCTATCTGAAAATATTCTACATGCTGCTTTTAGAAATTTG
AAGCGCATATGGTGTTCCTTGCGGAGACGCGCGCTCAGGGGAAGTGCATTTCCGAAAG
ATGCCTTTCCAGTCCCATATGCCCATCCCAAGATCATGCCCGGAGAGCAAAATGTCGCC
CCAGCCAGTTCGGACACATCTGTCTATTCGACCACCTAAGTATTGTCAAAGCTAGGGTTAAT
TGAAGATAGCTCTACATGTTATTAGTAGAGTTTTTAAACGTTGAGATACTAGTGAACGTA
TACACAAGAGCGGATAAAAGATGTCTTTAGTTGTCCAAGAACAAGGTTCTTCCAACACA

TTTTACGGTATGTTTATTATTACTAGTGAGCTATGACAAAATCGGCTAAAAACTTAAAAA
TATGACAGACAAGAAAGGAAATTCATTACCTCTTTAATCGTGGCGATTATTCGCTAACG
ACGTGATTAATATAATAATGATGTTCCCGGGCTGGACTAAGAACGTAATAATAAGGCTG
ATGAACAAATTTATGGTTTATGCATCAAAAAGGAACATGAATTTGGCATAAGCGCACATA
ATTACGGAACATTGCAATAGCGGTCGGAGGTAAAGTACCGGGAATGCTTTACAATGAATC
AGCTATTGGCGGATATTGACCAACCAACACTAAAATTTTATATCCTGCTCCGATTTTTGT
CTTGGCCGTGAAATCCATTATGCACATTTTACTAACGTTTATCAATAAGATTTCGTTTTC
CCGTCTAAATTTTTTTTACGCAGTTTGTGTAACACTAACGTTGACGGTAACATTAAGATCG
TTTACGCTTTGACCACTATCAAGGGTGTGTTGGTCGTCGTTACTCCAACCTTGGTCTGTAAGA
AGGCTGATGTTGATTTACACAAGAGAGCTGGTGAATTGACCCAAGAAGAATTGGAAAGAA
TTGTTCAAATTTATGCAAAACCACTCACTACAAAATCCAGCTTGGTTCCTTGAACCGTC
AAAATGACATCACTGATGGTAAGGACTACCACACTTTGGCTAACAAACGTCGAATCCAAAT
TGAGAGATGACTTGGAAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT
GGGTTTTCGCGTGTAGAGGTCAACACACCAAGACCACTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEQGSFQHILRLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPHTHYKI PAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFVGLRVRGQHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAACTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC
GACAGGTCGATGACTTGTAGGGCTCTTGACAGACTCTTCTCTACGCCAAAATCATTTTTTA
AAACCAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAAGAGGC
CACTAGAGGCCGGTGTGATTTGTGTAAACTAAGTGGACTAAGTCCCGTCGCTGTTATT
GGCGAATTGGTTAACGATGACGAACAAGGAACATGATGAGATTAAATGACTGCCAAGCG
TTTGGTAAGAAACATGGCATTCTTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG
AAATAATCTGGTGAACATTTTCTCATTTCTATCATCAACAGACTCACACATATATAC
ATGTATATATTTGTAACCTTTGTATATATCTTTTGTTTTTTGACCTTTTTCTCTCTATG
TTTTTCAGCCATACAAAATATGGGATTTTTAGCAAGAGAAAAAGTACATCTAAAAAAG
TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA
TGAACAGGATTTTCGGATATGGGAACAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCAGTTAGATACTC
AAATCGCCCAGTTAAACTTCCAGCTGCAAAATATTCAAAGAATTTGCAAAGATCAAACA
ACAAGCAACCCTCGTTAAGAAAACAGGCTTTTGAAGATTTTAAATAAACGTAAACAGTTAG
AAAATATGAAGGATTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCCAATACAA
ATGATAACTTACAGAACACAATGATCACTATAAACGCACTAAAGCAAAACAAACATGCCA
TGAAGGCTCAATACGGCAAGATAAATATCGACAACTACAGGACATGCAGGATGAGATGC
TGGATTTAATAGAACAAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAAACAGTG
GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG
AGGATTTCACTTTGCCAACCAGCGAAAACCTATTAGGTAACGATATGCCAGTTACTTAC
TAGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAACTTAGATACTGAAGACA
AAAATAAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHLKKVIVIGGSQDWLKHYSYKLFKAIMNRIFGYGNKKSHDQLLQESNQSMNQA
QQSLSNRISQLDQIAQLNQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL
DSQWSMTQAQLTNDNLQNTMITINALKQTNNAKQAQYKINIDKLQDMQDEMLDLIEQG
DELQEVLMNNSGELDDISDAELDAELDALAQEDFTLPTSENSLGNMPSYLLGANAPP
AFIDEEPFLDTEKKNKALESQA

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:
916-1295 (SEQ ID NO 67)

GGCAAATCAATTAATAATTCCTTTTTCTCTCTACCTTTGCTAATATTAATAAACCATAGTTGT
AAAGGGTACTTAATGCTATATTCCTGTTAAGTTTCCTATTTACCTTGTTTTTTTCCAATT
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAATCATTTTCCACCCACACATATATT
ACCTTTTGTGGGTGAAGAGAAGTAGTATTTTGTTTTTTCATGGGAGTGGAAGTCCTTTTT
AAAATAATCCGAGCAGTAGTGCTGTCTAGGCGGAGATTATTGAAAGTCGGCATTGGCTG
CAGCTAGCGTTTTGTTTTTGGTACTACCTGTCAAACCCGGCGTCTGCCTAGATTGCGCGG
AGGGTACGTTGAAACTTTTGCTTTCCACGTCAGTTTATAATATCAAAGCAGCAATATA

MAKFLKAGKQVAVVVRGRYAGKKVIVKPHDEGSKSHPFQHALVAGIERYPYPSKVTKKHGAK
KVAKRTKIKPFIVVNYNHLPLTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHOAGKNOWFFSKLRF

TAACAATAGAAAAAATACACACACATTAGATTGGAATTAGAGCTTAAGTGGGTACAAACT
AGGGCTAATAAAGAGGTAACGGTCGGTTCTCTACTAAGGTTTCGTATTGTGTGGCACC
GATTAAAGCACTTTTAAGCGGAATAACTCGAGTGGAATTTTATGTTTAGTTAGGTTTACC
TTGAATTTTTTTAAAAAAAAGAGTCAGACAGGCTCGCTCTTTCCCTACTAAATATTAGG
AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACCTCCAAAATTTAT
CTTACAAGAGCTATTAGTATCTTGGTTCTTCTATTTTCTTCGATTATTGGTGATTTTTC
CCGCTCTAGCCAAATCCGAGCGTTCCATCGATTTTTTGGGGAAAAACAGCATGCAAT
AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAACCTCT
TTTGCATATTTCTATTATAGATGAGACGAGAAACGGTGGGTGAATTTTCTTCAGATGACG
ATGATGATATTTCTTTTGGAAATTAGGCACCAGGCCTCCAAGGTTTACTCAAATACCGCCAT
CATCAGCAGCATTAACAAACAAATTTCCCACTACTTTGGAGGTTACAACGACCACATTA
ACAATAAACAGAGTAAAAATGATAACCACTGGTTAAACCACTGAATAAAGCTCAAGGTG
AAGCAAGCATGCTTCGTGATATAATAAACTTTTTGAACCACTGAAAGGGAAAGGAAAAGA
ATATTCAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT
TAAACAAGAATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG
GAAATTCGAAAAGGGAAAGTTATTACGAATGTAAAACCAACCGTCAACAACATTATCAACAA
ACACAACAACATAACGCCGAGATTCGTCCTCAGTTGCAATCGAAGCAAAACCTCAATCAC
CACAATCAAAAACCGTAAGATAAGTGATAATTTACTGAAAAAAATATGGTTCCCTTAA
ACCAAATAGGATTATTCGGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCTATC
AAATAATAGGCGCTGACCTGAGCACAATAGAAATATTAAATAGATTGAAGCTTGACTACA
TCACAGAGTTTAAATTTAAGAATTTTCGTATTGCTAAAGGAGCCCCCATAGGGAAGTCCA
TAGTTTCTCTACTTTTTCGATGTAAAAGACGTTGACCCTCGACAGGTTTCATAGATACTT
TGCTAGAGGATATAGCTGTTTTGATCAAGGAAATATCAGTTTCATCCAAATGAATCGAAAT
TAGCTGTCCCATTTCTCGTTGCATTGATGTATGATATTGTAACATTTTCGTCCCTAGTGCCA
TATCATAAATTTAGCAGCTGAAGGATGTTTTCTTTTATTTGCGAGTTTAATAAGAACTTATC
ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCTCAG
TTTTCCAATATGAACTGATAGACTATTTGATAATTTTCGTATTTCCTTGATCTCCTAGAAG
GTATATTAAAGGTACTGCACTCGCATCCTAAGCAAACCTTATATGGAATTTTTTGATGAAA
ATATTCATAAATCATTTGAATTTGTCTACAAACTAGCACTAACCATTTTCATACAAGCCAA
TGGTAAATGTAATATTTAGTCGAGTCGAGTCGTTAATATTTACTAGTATAATATTTAA
ATATGGACAATTTCTCAGATCTGAAATCCTTGATAAGCGTAGTTGGTGGAGAGATTGTA
TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGGCGACGTATAATGAAA
ATGTGGATACTACAACCTCTCATATGTCGAAGTACCATGACTTTTTTGGGTTAATCCGAA
ATATAGGTGATAATGAATTGGGAGGATTGATATCAAAGCTGATTTATACTGACCGATTGC
AAAGTGTCCCAAGGGTAATTTCTAAAGAGGATATTGGGATGGATAGCGACAAATTCACCTG
CCCCATAATAGGTTACAAGATGGAAAAATGGCTTTTGAAGTTAAAAGATGAAGTTTAA
ATATTTTGAATAATTTATATGATCTATGGAGACGATGCGACCATAGTAATGGAGAAA
TGCTCATCCACTCCTCTAAATTTCTTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTAC

TGGGACAAGACTCCCCGAACTTGGACCTCAGATGCCATCTTATTGAACATACTTTAACCA
TAATATATAGGCTATGGAAAAGACCATTTCAAACAATTGCGTGAAGAACAATCAAGCAGG
TAGAAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA
CAGCAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCTTTGAGGATTTACCAGAAATATATCG
AAGAAGAATTGAAGATGCAATTGAATAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAACTATTCTTGAGTCAAAATCATTCGATCTAACCA
CACTAGAGGAGGCCGATTCAATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)

MRRETVGEFSSDDDDILLEGTRPPRFTQIPPSSAALQTQIPTTLEVTTTTLNNKQSKN
DNQLVNQLNKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELQVKHLQELAKLKQELQK
LEDEKKFLQMEARGKSKREVITNVKPPSTTSLSTNTNTITPDSSSVAIEAKPQSPQSKRK
ISDNLKKNMVPLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITFEFKF
NFVIAKGAPIGKSIVSLLLRCKKTLTLDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFCDLIRIYHHVLKVPIHESNMNLHVEPQIFQYELI
DYLIISYSFDLLEGILRVLQSHPKQTYMEFFDENILKSFEFVYKLALTISYKPMVNVIFS
AVEVUNIITSIIILNMDNSSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTTL
HMSKYHDFGLIRNIGDNELGGLISKLIYDRLQSVPRVISEDIGMDSKFTAPIIGYK
MEKWLLKLDVLNIFENLLMIYGDATIVNGEMLIHSSKFLSREQALMIERYVQDPSN
LDLRCHLIEHTLTIIYRLWKDHFQKQREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDQASYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKFQEM
ARTILESFSFDLTTLEEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)

CTCTTTAAATATTCTATGTACTTTGTGCAAACATCATTGTGCATCACATAAAATGCATTCCT
ACTATTACTAACTTGAACCTTCACTTCACTGGAAGAACTGGGTTATTCAAGGTAAAGAAAT
CATTTGTTTTCGCGCAAGTTTCGTCTGACAAGAATTTTTTATTATTATTTCCCACTTTTC
ATCGAAGGAAACGCGTCAAATCCATTCTGTTACTACGCGCAATCTGCGTTATTTCTTTT
CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCTTTTGTATGTTAAATTAA
AAGCGACTGAATGAAGTGCACACATTTTTTATTTCTTCTTGATTTTCTTTCTATTTTGT
TTTGCTTCTCTTCTGTGCGACAACGTCTCAACTGTACTCACCATTAGTATTCTCGAAGGC
TTTAGCAGACTTGTGAATAATTAATTGCCCACTTTGATCAAGAAAGATATTCGCAGCACA
ATACAATAATAACATTCAAATGGCAATCAATGGTAACAGTATTCTGCCATAAAGGATA
ATACCATCGGTCCATGGAACTAGGTGAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC
AGCTTGCTCGTAATGGATCCACAGGACAAGAGGCGGCAGTTAAGGTAATATCAAAAGCAG
TATTCAATACCGGTAATGTGACGGTACTTCGATTGTTGGCTCCACCACCCAGATGCTC
TACCATATGGTATAGAACGCGAAATAATCATTTATGAAGTTGTTAAACCACCCAAATGTGT
TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTTAGAAATACGCGG
AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCCTCTGCCAGAGCATGAAGCTA
TCAGGTTTTTTAGACAAATTATTATTTGTTGTCGTACTGTGTCATGCGTTGGGTATTGTCC
ATCGTGATCTAAACCGGAAAATCTATTATTAGATCATAAATATAACATCAAGATTGCGAG
ATTTTGGTATGGCTGCTTTGGAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC
CACATTATGCTGCACCAGAAATTGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG
TGTGGTCAATGCGGTGTGATCCTATTGCGCCCTTCTTACTGGTCGGTTACCTTTGACGAGG
AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCCTT
CTGATGATGAAATTTGCGGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC
CTGAAAGAAGAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA
GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAGAGAAGACACATATCTCACGCCAT
TATCAGAAAGTAATTCTTCTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC
ATGGAAGAGATCCTGAAGGAATTAAGGAAAACTAAGAGAACCTGGCGCTAATGCAGAAA
AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAAGC
AACAGCAAGTTAAGAAGAGGCAGTCAATTAGTAGCGTTTCTGTTTCCCCATCTAAAAAAG
TATCGACAACTCCACAACGCAGAGAAATAGAGAATCTTTAATTAGTGTAACATCTTCTC
GTAAAAAGCCAATATCTTCAACAAATCACTGCCTCCAGTGCCTCCTCCAGCAATCTAA
CTACACCCGGTTCTTCAAAACGCCCTTCAAAAACCTTCTCTTCAAGAAGAAATATTCTA
CAATCGTTAACCAATCTTCTCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA
ATGTGGAAGAAGTAATCAAAAAGAGCCTCTATCTTTCTACTACCAAGAAGAACAAAAGAT
CTTCTAGATCTATCAAGAGAATGTCAATTGATACCAAGCATGAAACGTGAATCGGTGACAA
CAAAATTAATGTCAACATATGCGAAATTTGGCAGAGGATGACGATTGGGAATACATTGAGA

AGGAAACAAAGAGAACGAGCTCAAATTTTGCAACTTTGATAGATGAAATTTTGTAGTACG
AAAAGTACGAACAAATAAGGAAAAGAGAAGGAAGAGCTAGAACGTAAAGTGAGAGAAAGCAA
AAGCACGTGAAGAGCTGGAACGTAGAAGACGTAAACAAGAAGAAAAAGAACGTGCAAGAA
AATTACTAGAAAAGGAAGATCTGAAAAGAAAACAGGAGGAACTCAAGAAGCAAATTGAAA
TTGATATAAGTGATCTAGAGCAAGAGCTGTCCAAACACAAAGAGGAAAAACTGGATGGTA
ATATTAGATCTATCTCTGCTCCTATGGAAAATGAAGAGAAAAATATCAATCATTTGGAGG
TTGATATTGACAATATTCTCCGTCGCCGCAACTTTTCTTTACAACTAGACCTGTGTCAA

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAACCTGAGGAAGTAAGTCCAGTGAACCAA
AGAGAACAGAAAATGAAAGACTTACAACAGAAAAGAAAATTTTAGAAAATATCAGAAGAT
CAAAATTTCTTGGGTTTCATCATTTAATATCGATAAAGAGTTGAAATTGTCTAAAAATGGAAT
ATCCAAGTATAATTGCACCACAAAGATTGTGAGGAGCGAGTGGTGTGAGATTCTAATG
ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAAGGATA
GTACCGCAACAACCTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG
TACCACAATTTACTAGAAAATCAAGGCATTTTGTAGTGAAGTCCAATAAAAGGCTATCTGTCC
TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTTGGTTGATATTTTAAAAACGGTA
ACCTTGATGTCAATAACCAACAAAGCCAAAGAAATTCACACACCAAGAAAGTGCGGATGATT
CAGAAATTTCTTTTGAAGTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTTCAAGC
ATGAGAGATTGTACGATGTGCGGTGATTCCACTATCAAAGACAAATCCGCGTTAAAGCTGA
ACTTGTCAGATCGTTTAAATGGATCGAACGAAGCGAAACAACTGATAACTTACATCTTC
CGATCCTTCTCCGCTTAATGGTGACAATGAATTCGCTAAACAGAATAGCCAAAGGGTG
ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG
AAAAGGAAGAAGAAAATGAGGAAAAGGAAGAGAAAAGCCAGAACAACACAAACAAGAAG
AGGATCAAGAAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG
TGCAAAAAAATTAGGGAAAAAAATGCTGGCTCGCAGGCAAAGGATCATTCAAAAAGATCACT
TAAAAGAGCATAAGCAGGATAAAAAATACAGCAATTGGAATGGTTCTTCTTTAGAAAAT
TCTCAAAATCTTTCGGACAAAACAATGGAATTGTATGCCAAGATTCTGCAAAACAAATTGT
TTAATGGTTTAGAGAAGCTGTTGCGTGTTGGACTCAGTATGGTTTAAAAAATATAAAAT
CGCACCCCAACAATCTGACCTTAACGGGTAAACTATCGAGTGATAATATATTCTCACTAC
GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA
AGAAAGTTTCTGGTTTCATTCAAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTC
TGAATAAGGAAGGCGTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINNSIPAIKDNITIGPWKLGETLGLGSTGKVQLARNGSTGQEA AVKVISKAVFNTGNV
SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN
LLVERGPLPEHEAIRFFRQIIIGVSYCHALGIVHRDLKPENLLLDHKYNIKIADFGMAAL
ETEGKLLLETSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT
LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLQKYPsirDSKS
IRGLPREDTYLTPLESNSSIDATILQNLVILWHGRDPEGIKEKLREPANA EKTFLYALL
YRFKCDTQKELIKQQQVKKRQSISSSVSPSKKVSTTPQRRRNRESLISVTSRKKPIF
NKFTASSASSNLTPGSSKRLSKNFSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK
RASIFSTTKKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS
SNFATLIDEIFEYKEYEQIRKEKEELERKVREAKAREELERRRRKQEEKERARKLLEKED
LKRKQEELKKQIEIDISDLEQELSKHKEEKLDGNIRSIAPMENEENKINHLVDIDNIL
RRRNFSLQTRPVSRDLPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS
FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNVGSQKLDSTATAP
VSDGRLRKISEIRVPQFTRKSRHFSSESNKRLSVLSMYSTKESFTNLVDILKNGNLDVNNQ
QSQRIPTPRSADDSEFLFETVNEEA EYTGNSNDERLYDVGDSTIKDKSALKLNFADRFN
GSNEAKQTDNLHLPLPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSSTEKEEENE
EKEEKKPEQHKQEEDQEKREKVDDMEPPLNKSQKIREKNAGSQAKDHSKDLKEHKQD
KNTAIGNGSF FRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNLTL
LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKKVS GSFKAVKKLVNEVENVLNKEGVL
QK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATGCGTAACCATTTTGA CTACCGCTTCGTATGCTTTCTTGCACTTTGTG
GAGCTACTCATACAATAGCTTATAATCTGTGTAGTCAA CTATATACTAGGCAAATTA CT
AGTAAATGCAGTATT CATATGTCTCAAACCGTTTTTTTGCAGTATGTTATTGATCCATCG
AATCAAAATTTTTTACC CGCAAGAGAAAAAAGATCTTACTATTTTGTGCTTATGAAAAA

TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAAATTGGC
ACATCCTTGGTTGACACTTGTCTATTTATTTAAAAGGTTTTAAAAAGTAGTGTTCAGCAGT
TCTATCATATTTTTTTTATTTAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA
TTTAGGGTGGCGTTAAATAAACGAGAGAGCCCCAAAAATATAACCAAGATAAAGAAAAATCA
ATCATAAAGTGAATTCAAAAATGTTCATCGCAAAACCTCAATGATAATCCAAAAATACAT
CCTCAGCAGCTGAAGATAAGAAGAAACAACTTCATCCTTAAAGTTGGCACCAATACCAA

CCACATCGCCATGGAAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC
TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTTCGGGGTCAATTAAATTAA
CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA
CAAATTCAAAGTCAGGAAAGAACTCTAAAAATTCCTAAGACTAATAAAAAATGAAAAAGC
GTGGCAAATATAATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT
CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA
ACATACATTCAGCTCAGGAGCAATGCCAATGGGAATATAAAGAGGATAACAAACAACA
ACAATTCAAACCAACGGTAGACAATCAAGAAATTTATCAAAACAGGAATGGCAAAACAAGAT
ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAATAATT
ATCAGGCTAGACCTGAATATATTTCCCAATGCCAGCCACTGGTTGAACAACAATTCAGAA
ATAGCTATAAACAACGTGCATACCTCCGTCAACAGCAGTATTATAATAACATCAACTATC
AACAACAATTGCAAACACCATATTATTTACTCAATGGAACCTATTTTTAAATCTATCGAAA
GTATCAAAAACCAAATTTGAATTCATTTTAGTGAAGAGAACTTGAAAACAGATGAATTTT
TAAGATCTAAATTTCAAAAAGCCAATGACGGATTTATCCCCATGAGTTTGATAGGGAAAT
TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA
GAGAAGTTTTTACAACATAAAGAAACAAACCATTTGGAAATTGCCCTTGGAAGCATAGAAG
GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAAAACCTATTTTATTAGGCGG
AAAATTGGGCTGAATACGCTATGGAAAGTAATTTTGATGAAAATGATGACGAAACTGAAA
AATACAACATTGAGAACTATTGGGACCGAACGATTTAGACAATTATTCTTATATGGGCT
ATCCAAACTTCTTCCCAGTAATGAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG
AAATTAGCAGGCAGTTTGAACAAAACCTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLDNPNKNTSSAEDKKKQTSCLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT
AKPSKNGSGSIKLTSTNKWTPITPSVIIISGSKDTNSKSGKNSKNSKTNKKMKKRGKYNNND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKIRITMNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNSRNSYKQLS
YFRQQQYNNINYYQQQLQTPYYYSMEPIPKSIESIKNQIEFYFSEENLKTDEFLRSKFKK
ANDGFIPMSLIGKFYRMVNLSLGGDPNLLIASMREVLQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNDLDNYSYMGYPNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCTGTTCTGTTCCCTGTTCCAGTAGAATCTGAGACGGC
TTTTGTGCCATCAGCATTCACAGCACCACCGGTGCCAACAAAGAAGAAATCAAAAAATAA
AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTTAATGAAGGCAGAGATAAGTCATC
TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC
CTCTGATTAACTTTCTGTTAGTCTTTTGGTTTTGTTCATAGCAAAATTAATATATATA
TATATAAGCTTGTCTTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA
CCGAGACTTTTTTTTCAAAGGCACGCGTGCTTTTTTTGTTAAGACAATAGATATTTTAGC
ATTCAGAAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA
GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT
TTTGCCTGTTTGCTTCTTTACGTTGGCTGAAAACAGCGCAAGAGCTACGCCGGGATCAG
ATTTACTCGTTCTAACAGAGAAGAAATTTAAATCATTCATCGAATCTCATCCGTTAGTCC
TCGTGAGTTTTTTGCTCCATGGTGTTCATCTCAGATCTTACGCCCTCACTTAGAAG
AGGCCGCTCTATTTTAAAGGAGCATAACGTCCCAGTTGTTCAAATTGATTGTGAGGCTA
ACAGTATGGTTTGCTGCAACAAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA
ATGGTCGTATTTTGTATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC
AGTACATGATTCAGCTATACGAGGCTTCTGTCAATTTATTTAAATTCGAAGATGAAATCC
AACCATACTTGGAAAATGCAACTTTACGAGTAGTAATAAACAGAGGCTTGACAGGCTTGA
ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTATCCCTTC
TAGATTGAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATTCGTGT
TTGATGGAATGTAGACTCTTTGGTCGGAATTCGGTTGCTCTAACTCAGTGGTTAAAAAG

TGGTAATTTTACCTTACTTTACCGACATCGAACCTGATCTCTTCCCCAAGTACATTTCTA
GCAATTTGCCGCTTGGCTTACTTCTTTTATACTTCTGAGGAAGAATTGGAAGATTACACTG
ATCTTTTCACGCAGTTAGGTAAGGAAAATCGTGGCCAAATAAATTTTCATTGCATTAACT
CTACAATGTTCCACACCACGTTAGATTCTTAAATATGAGAGAACAGTTCCCATTTATTTG
CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACCAGAAGAAGAGT
ACGCGAAATTAGAAAAACCACAACCACTAGACAGAGATATGATCGTTCAGTTGGTAAAAG
ATTACCGTGAAGGTACTGCCAAGCCAATTGTTAAGTCAGAAGAGATTCCAAAAGAACAAA
AGTCCAATGTTTATAAAATAGTTGGGAAGACACATGACGACATTGTTTCATGATGATGACA
AGGATGTCCTTGTCAAATATTACGCGACATGGTGTATTTCATAGTAAAAGGTTTGCCTTA
TTTACGAAGAAATTGCAAATGTCTTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTGA
TCGCCGAAGTAGATTACAGGGGCAAATGATATCTTAAGTTTCTGTGACAGGATATCCAA
CCATTGCTTTGTATCTTCCCGGAAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAA
ATTGGAAGATGTTTTTCAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGG
CAATTTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)

MQVTRFISAIVSFCLFASFTLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNVPVVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG
QVYRGVKITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLDSEDKSLSIHLNPTTPEILFDGNVDSL VGNSVALTQWLKVVILPYF
TDIEPDLFPKYISSNLPLAYFFYTSEEELEDYTDLFTQLGKENRGQINFIALNSTMFPHH
VRFLNMREQPLFAIHNMINNLKYGLPQLPEEYAKLEKPQPLDRDMIVQLVKDYREGTA
KPIVKSEEIPEKEQSNVYKIVGKTHDDIVHDDDKDVLVKYYATWCIIHSKRFPAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)

GGGGCAAATGATATCTTAAGTTTCTGTGACAGGATATCCAACCATTGCTTTGTATCCT
GCCGGAAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTT
GAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGGCAATTTATGATAAATTG
CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA
ATAAATAAAGCATATATAATGCACATTTTAAACATCTGATTACTCGCATCGTTTCTGGAA
GAAATAGCTAATATTCTGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA
TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA
CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTCGTTTTCAATCACATTCTAG
TTTACAGTAATTGAGTCTCGATGATGTTTAATATTTACCTTTTCGTCACCTTTTTTTTCCA
CCATTCTTGCAGGTTCCCTGTCAGATTTGGAAATCGGTATTATCAAGAGAATACCGGTAG
AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTTATTATACAGGATCTT
TATTAGAATCGGGAAGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG
AACTTTGGCGTTGGCAGAGTAATTAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG
CCGAAAAAGAAAGCTGCAAATTTCAAAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCAG
GCGTCATTCTCCAAGTGCTGATTTGGTGTGTTGATGTGCAATTGGTAGACGTGAAATCAG
CCGCTAG

YDR519W, 136 aa (SEQ ID NO 78)

MMFNIYLFVTFSTILAGSLSDLEIGI IKRIPVEDCLIKAMPGDKVKVHYTGSLL ESGTV
FDSSYSRGSPIAFELGVGRVIKWDQGVAGMCVGEKRKLQIPSSLAYGERGVPGVIPP SA
DLVFDVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)

CGAGCTTGCCAGCATTCCAATGCCCATCGTATTGTACTCAATGGTGAACTTACCACCAT
ATTGTTAAAAGCTATTATTTATGATTTTTACTTACCAAACATTGAAAGGAGACTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATTCTAACGCA
TGCATCTTGAGCAATGAAATCATGCAACCTAACATTTGAGGTTAATATATGAGAATTAAC
TAGCGTTGAGGAGGTACTGCAATTTAAAAGACCGAAGAATTATCGATGCAAGGAAAAATG
GGTCTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAATATCACAT
ACTTTTCGCTTCTATCTCGATGCGTTATTACAAGAAAATAGTTTTACTAACAAATTAACA
AAAATTAATAATAGTGTAATAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCAGCCA

CTGGTGCTAAACGTGCTCAATTCAGAAAGAAGAGAAAGTTCGAATTAGGTGCTCAACCAG
CCAACACAAAAATTGGTGCTAAGAGAATCCACTCTGTGCTAGAGGTGGTAACAAGA
AATACAGAGCTCTAAGAATTGAAACCGGTAACTTTCTTGGGCTTCTGAAGGTATCTCCA
AGAAGACCAGAATTGCTGGTGTTGTTTACCATCCATCCAACAATGAATTGGTTAGAACTA
ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTGAGACAATGGTTTCG
AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAGAACTGTTG
CCAAGAGCAAGAAGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT
CTTCCGTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGATCTCTTCCAGACCAG
GTCAATCCGGTAGATGTGATGGTTACATCTTGAAGGTGAAGAATTAGCTTTCTACCTAA
GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)

MGISRDSRHKRSATGAKRAQFRKKRKFFELGRQPANTKIGAKRIHSVRTRGGNKKYRALRI
ETGNFSWASEGISKKTRIAGVVYHPSNNELVRTNTLTAAIVQIDATPFRQWFEAHYGQT
LGKKKNVKEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81)

ACCCTATATGGGAGGACAACCTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG
TAGAAGCGGAAAGAGAAGGAGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT
GGATTTCCGAGACATCGTTGGCATTGTTGGCCCCGTCGAATTAAATCTTTTGGCCTGAAAAG
AGATCCATGACGGATGGGGCCGGGGCAATACTATGGTTCGAGCGGTGGCCAGTCTGGAAG
AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTCGGGGAGGTTA
TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATT
TTTCATGGCTCGGATTACTTCCGTAAGTGTGGCTAAATCGAAATCTCGGCCTGCTGAGA
GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA
ACATAAGAACGGAACACGTCATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC
GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC
GTCAGCAGCAGCAGACCAGCGTGGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG
CTGCGCTTGCCCATGCCGACACTATAGCATAACATGTGGTATCAGCATGTGATGCCACGCC
GGTTGCCAGTAGAGGGCCGCCCTGCTATGTGAAATGGCTGGCGTAGCATTGTACCAGGACA
GGCTCTTCTTACCCGCGCAGTTCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA
CCAGCCCAGAAGATGAAGTGAATGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG
CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAAAGTGGAAGGTATTCTTGCAGGAGA
TGGATACGATACTACCGGCGAGCCGCCATTAAAGCTGCGCGACTTCCCGCAAATGACCAAGG
CTATGGGCATAGCATTGATGCAGCAAGATGAGCAAGCAGCTGCCCTGGCGTTGTTTGGAC
GACAGCCCCCTAGTGATAAAGAACGAATGGTCACTACCGCTACTACTGGCTGGTGTCTTT
GGCATGTTCCCGGCCAGCGCAGGCGGACGTGTGCTGGCGGAGTTCCGTCAAAGTTATC
GCGGGCTGCCGCTGCTGGATGCCGAAGTATGATAAAGAGAAGAGGATTTGAAATCAACA
CATAA

YER153C, 254 aa (SEQ ID NO 82)

MLTITKRLVTTDVRSRILLSSLNGKMSDALALLRQQQQTSSVDVELLHTMLARAAALAHAD
TIAYMWYQHVMPPRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNDRRTSPEDEL
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPQPPLRLRDFPQMTKAMGIALM
QQDEQAALALFGRQPLVIKNEWSLPLLLAGVLWHVPGPAQARRVLAEFRQSYRGLPLLD
AELVIKRRGFINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83)

GGACTAGAAGCCAAAAGCCAGAGGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC
TGTTAAGGGGATATGTTGCAACTTGCAGGGGGCGGCACAAAATAACATAGAAACGTAGTA
AAGAGGGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAAACCATTGACGTAGAAAT
TGAAAGAAGGAAAGGTATACGCAAGCATTAAATACAACCCACAAACACAGACCAGAAGCAC
TCTAGACGGAGAGTAACTAGATCTACAGCCCCTGGAAAATCGTTTGGTCAACTTTGAGGT
TCCGGTCGTCCCCCTCTTGATCTGAAAGGTCTTTCTCTAAATCTATATTAACGTATAA
ATAGGACGGTGAAATTGCGTTCTACTTCTCAATTGCGTTTGATCTTATTTAATCTCTCTC
TAATATATAGAAAAAAAACCATCTGATTAAATTCGATAATCTCAAACAAACAACCTCTCTC
AAAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAGGATTCGGTGAAAAAGCTT
CTGAAGCTTTGAAGCCAGACTCTCAAAGTCATACGCTGAACAAGGTAAGGAATACATCA
CTGACAAGGCCGACAAGGTGCTGGTAAGGTTCAACCAGAAGACAACAAGGGTGTCTTCC

AAGGTGTCCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTCG
AATATGTTTCCGGTCGTGTCCACGGTGAAGAAGACCCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRKGFGKASEALKPDSQKSYAEQGKEYITDKADKVAGKVQPEDNKGVFQGVHDSA
EKGKDNAEGQGESLADQARDYMGAASKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCCTTTTTCGGCAGAGTCGTGGACACCTTGGAAGACACCCT
TGTTGTCTTCTGGTTGAACCTTACCAGCGACCTTGTCGGCCTTGTCAGTGATGTATTCCT
TACCTTGTTTACGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTCAC
CGAATCCTTTTCTACCTGCGTCAGACATTGTTGTATTTAGTTTTTTTTTGTTTTGAGTTGT
TTGTTTGAGATTATCGAATAATCAGATGGTTTTTTTTTTCTATATATTAGAGAGAGATTAA
ATAAGATCAAACGCAATTGAGGAAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTTA
ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG
ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCCTAGAGTGCTTCTGGTC
TGTGTTGTGGGTTGTATTAATGCTTGCGTATACCTTTCCCTTCTTTCAATTTCTACGTC
ATGGGTTTTTTTTCCCTTCCCTTTCCCTTTCCCTTTTCCCTTCTTACTACGTTTTCT
ATGTTATTTTGTGCGCCCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT
ATTCTAGTCTTGCTATTTTACCAGCTCTGGCTTTTGGCTTCTAGTCTTGTCCCAAGAG
CCAAGGGCCCGTCAACACGTCGTCATTGCTACCGCCAGCTGGCACCCACACATCACCGAC
CCTTTTTTCCATTTTTCGGCTGGGCGTTAGTGGGATCCGCCCGCTCCCGGAGATTTTCA
CTTGGAATTTGCGCGTCCCTTTTTTTCTTCATTTCTGACTCCCCCTACCTTCTCCCCT
TTTCTGTGTATCAAGAGGAAAAGAAGGAGAACTCCGAAAAATACCGAACAAAG
AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSFNFYVNGFFSFLFLFLFLFPSLLRIFYVILCRPLQVATYPLNRCQQYSSLAIF
TASGFWLLVLVPRAKGPSTRRHCHYRQLAPTHRPFFSIFGWAVSGIRPLPEIFTWICASP
FFLHSLTPPTFSHFVSUYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCCTCCGTACGTCACAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT
CTATCCTTTTGCATAATATTTTCGTCACCATTATCTTGTTGCGGTGTTTTTATTTAAAC
AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAATTCAAAAAATGGCTTTCATG
GATCGAGTATTTGTTTGTGCAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC
TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCCTCGGA
AGAGTTAACTTACGCGGGTAAATCACTTGATGCGGTATATTCTCTATACGGCTAATA
GATGAATCAGGGTGTTTTTAAAGTGCGTATAAACCTTTTGCTATTTTTCGTTTATATAAT
GGCGTTGATAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT
AAAAATACAAAAAGTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC
TGCTTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGTCCCTC
CAAACGAGGGCCCCCTCGGTGCTTTTATCTGGTTGCATCGTTTATCGATTAAACGAACCCA
TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG
AGAGGCCCCAGGACGCTAGTTCTTCGTCGTTGCTTTCATCGCCGCAAGATCAGAAAGT
ACAACAAAGTTTTTTTATAATTACGCATGGGATAATGTTAACTCAAGGAGTATCTGAGTG
GTTTAAAGAGGGCAATCTGGCCTTGCGGGCAGTAGCTCATCAAGTAATATCTTGGGCACTC
GCCAAAGAGCTCAGTCCACAAGTTCCTTGAAGTCTTTAAAGGGGTCTCCTCACCTCTT
CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGGTTTCGT
TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCGTGACATATAGCATGGAATCCGTTA
TTGAACGCAGCAAAAATTATAGTGATTTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA
CCATTTACCCGCGCAGCAGTGGAGTTATCAGAACTGTTTGTGTAGATAACTCATGGCCCCG
ACAAGTGGATTATTCTATTTTCAGTACCCAAAGCCGAGCTATTGGTTTCAGGCCCC
CTATAAATATTTCCATTGTACCTCTTTCGAAAGGTTTGAAATTGGGCTCAATCAAAGTCG
TATTATTTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGGC
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA
ATGGTTGCTTTGTAAATAACCCCTTTTTTCAGCCTGATCATTCAATCCAAGACAAGTGGG

AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACGTGTGTGCAAGATTGTGATG
TCCGCTCTAACATTAAGGTTCCGCATAAGCTCAAATTTTTTCATCATCCTAATTAACCCAG
ATGGTCATAAATCTGAGTTAAGAGCGTCCTTACCGATTCAACTTTTTATTTCACCATTTG
TGGCACTTTCAATAAAACCATTTGTCATCCTCGAATTTGTATTTCGCTTTTTAGCACCCTA
ACCAGAAAGACGAAAACATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG
CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCCCTACCA
TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG
GTTCTTTCACTCGCACGGCTGTGGAAACGCTCGGAACATGTACTCCTTTGGGAAGCGAAT
GTTGACTGTGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA
TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCTGCCGCTTCCA
GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCAGGAGAGAATCTTAC
CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC
CTGTTTTTACTTTCAAGATCCCAGCCCCAAGCGTGTGAGCCCATGAAGTGTTACCAGTGC
CCTCGGGCTTAAATTATCCAGAGACTCAAACCTGAACAAGGTTCCATCGTATGGCAAGG
CAATGAAATATGATATCATTGGTGAGGACCTTCCTCCTTCCCTACCTTGTGCGATACAAA
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCAGGAACCTTCGACAACATTGTTCAT
CTTCTATACCAACTAGCTTTTCATTCTCTAGTTTTATGAGTAGCACTGCTTCCCCATTTT
CCATAATTAATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACACTTAATGAGT
TAACCTTCGAAAACCTTCGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC
GGAGGGCTACTTCTTTAGCTGGGTTTATGGGAGGTTTTCTATCAAAGGGTAACAAACGAT
AG

YFR022W, 733 aa (SEQ ID NO 88)

MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPPNEAPSVLLSGCIVLSINPEMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLS SSPKIRKYNKVFN YAWDNVNLKEYLSGLRGQSG
LAGSSSSN ILGTRQRAQSTSSLKSLKGSSSPSSCTLDKGN YDFFSAILPGSLPESVES
LPNC FVTYSMESVIERSKNYS DLICRKNIRVLR TISPAAVELSETVCVDNSWPKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLSIKVVL FENYQYCDFFPPVIS ENRQVTELNL
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNCVQDCDVR SNIKV
RHKLKFFIILINPDGHKSELRASLP IQLFISPFVALSIKPLSSSNLYSLFSTTNQKDENS
SQEEEEEYLF SRASVTGLELLADMRSGGSVPTISDLMT PPNYEMHVYDRLYSGSFRTA
VETSGTCTPLGSECSTVEDQQQDLEDLRILRTKIRNQRDNLGLPPSASSAAASRSL SPL
NVPALGPN SGVPGVHNSVSPVLLSRSPAPSVSAHEVLPVPSGLNYP
ETQNLNKVPSYKAMKYDIIGEDLPSPYCAIQNVQPRKPSRVHSRNSSTLSSSIPTSF
HSSSFMSSTASPI SI INGSRSSSSGVSLNTLNLELTSKTSNNPSSNSMKRSPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT
ATTTTGACTCTGTGGAGCATACAGCTACCCTAAATAGGATTGTGGGGACAAATATGGAA
TGGATCAAACGTTCTTAGGATTGTGGTGGTAAACTTGTAATAATCCAAGCTGAGATCTT
AAATCCAGCAAACCTTCGCCCATATTTATTCTTTTATAACAGAAGAAGAGACTATATTCT
CAAAACCTCGTATATTTATATACATATCCTCCAAACAACTCCCAAGTTTCACTTTCTCTG
GATTTACCTTGGCATTCCTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA
TGATATCACAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA
AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC
GAAAAAACA TATTACAATCATGTGCGGTGCTGCTGCTGCATCTGCTGCTGGTTATGACA
GGCACATCACTATCTTTTCCCCGAGGGTCGTTTATATCAAGTAGAATATGCCTTTAAAG
CGACTAATCAAAC TAACATAAACTCACTAGCGGTGAGAGGTAAAGATTGTACAGTGGTGA
TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAAC TACTGTTTCGTATATTTTTT
GTATTTCAAGAACAAATGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG
CCCTAAGAGCCAAGGCTGAGGCTGCAGAAATCCGTTATAAATATGGTPTATGATATGCCAT
GCGATGTATTGGCTAAGAGAAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA
TGAGACCATTAGGTGTTATACTCACATTTGTTTCGGTAGATGAAGAAATGGGTCCCTCCA
TTTACAAAAC TGAACCTGCAGGTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA
AACAAACAGGAGATCACAACAAACTTAGAAAACCATTTCAAAAAGAGTAAATCGACCATA

TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGATTGACGCAC
TGGGTACCGAATTTTCAAAGAATGACTTGGAAGTCGGTGTGCTACAAAGGACAAATCT
TTACCTTGAGTGTGAGAACATCGAAGAAAGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)

MSGAAAASAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKR
MANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDPAGYVVGYKATATGPKQQEITT
NLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVGVATKDKFFTLAEN
IEERLVAIAEQD

YGL031C, 968 bp, CDS: 501-968 (SEQ ID NO 91)

CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT
TCATAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG
AGAGCTTCAGATAGCCAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTGTTC
GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCCAATGAAAATGCTTCATTAC
ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG
AACCTAGTAAATGAATCTGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC
TACAATTTTGCGAACGCCTGAACAACCATGCGGATTACCATTATTTATATTGACAAGATG
GCTACCTATGAAAAGCATAGACTTACTAACATTTTTTTTTTCAAATATGTTTGAACAAACG
TGGATTATATAGTGATAAAATGAAGGTGAAATCGATTCTTTTTCAGGTGCCAAATCT
ACCCAGGCAGAGGTACCTTGTGTCCGTGGTGACTCCAAAATCTTCAGATTCCTCAAACT
CCAAATCTGCCTCTTTGTTCAAGCAAAGAAAGAACCCAAGAAGAATCGCTTGGACTGTCT
TATTCAGAAAGCATCACAAGAAGGGTATCACCGAAGAAGTTGCTAAGAAGAGATCTAGAA
AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA
GATCTTTGAAGCCAGAAGTTAGAAAGGCTAACAGAGAAGAAAATGAAGGCCAACAAAG
AAAAGAAGAAGGCTGAAAAGGCTGCTAGAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC
AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTCCAAAAGGTTGCTGCTACTT
CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92)

MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASLQKQKPNPRRIAWTVLFRKHHK
KGITEEVAKKRSRKTVKAQRPITGASLDLIKERRSLKPEVRKANREEKLANKEKKKA
AARKAEKAKSAGTQSSKFSKQQAQKAFQKVAATSR

YGL032C, 764 bp, CDS: 501-764 (SEQ ID NO 93)

CTCCCATATTTTTTTTATTCACAGGCTAGACAATGGTAATGGTGCTTTAGATGATTTCA
GGATTACATTTCGCACAATAGATAAATGACTAATTTTCAAGAATTTGTTTCAACCTGCCG
GCATTTCAGTTATTATAAGTTATTGTTTGATGGTAAACTTCGCCATCACCGGTTGCTGCG
TTTATTGCAAAATTAAGTAAACCATGTAATTTCCGAATACGGTAATTACACGCAGTTTGA
AATTTGACATGCAAGTTTAAACAAAAAACTTCTGTCCGCATCTAAAGCTTAATTAAGGGA
CTGTTTCATACCTTCAGATCCAATATACTGAATATCAGGCAATTGATTTCCCTTGTAAT
ATACAATATAAATAGTTGTAAGAAGAGGTGATATGTTAAGTTTCCATTTTGACGTATTCC
TCATTCTAGAATGATTGTAAGCTCTCAACAGTCACTTGTGTGCCAAAATATTATACCTAC
TTCATACATTTTCAATTAAGATGCAGTTACTTCGCTGTTTTTCAATATTTTCTGTTATTG
CTTCAGTTTTAGCACAGGAAGTACAACTATATGCGAGCAAATCCCCTCACCAACTTTAG
AATCGACGCCGTACTCTTTGTCAACGACTACTATTTTGGCCAACGGGAAGGCAATGCAAG
GAGTTTTTGAATATTACAAATCAGTAACGTTTGTGAGTAATTGCGGTTCTCACCCCTCAA
CAACTAGCAAAGGCAGCCCCATAAACACACAGTATGTTTTTTGA

YGL032C, 87 aa (SEQ ID NO 94)

MQLLRCSFISVIAVLAQELTTICEQIPSPLESTPYSLSSTTILANGKAMQGVFEYYK
SVTFVSNCGSHPTTSKGSPISTQYVF

YGL043W, 1430 bp, CDS: 501-1430 (SEQ ID NO 95)

TCGGGATGGTGGGTGTTCTGTACCCCGCATTACACCGCTCTGCCTATTCATTTTATC
GTTTTCTGCTTTTCTTCAATGTATTGATAATTAACGTGTCTATGTGATGCTATTGGTAT
ATAGCCTTTCTTGATATCCCTCTAACAATTATTACAAGTGTTTCTGTTTAAAGCAAGTG
CTAGAAGTGAAGTCTGTTCTCTTAGGAAATCTAAACGCAAGATTTCTCTTATGGTGATTG
TAACAATTATGAGATACTTCACTAGCCACCTTAACCTTACGGACCTTCTTTTGAACGA

TGCTTCGAATGACAACGCCTTTTGTATATATAATATCCAATTTTCATTATAGGGAAATTTT
CAACTCTTACCCGCCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC
GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTACAGTGTAAGTACAG
TCCGCATAAGAGCATTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG
AAAAGAACAAAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCTTGGATAAAGAAT
TCGTCCCCACTGAAAAGTTACTGAGAGAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA
AAAAATCCACTAATGTAGAGATCAGCAAACTCGTGAAGAAAATGATTAGCTCTTGGAAAG
ACGCAATTAATAAAAAATAAGCGTTCCAGGCAAGCACAGCAGCATCATCAAGATCATGCGC
CAGGCAATGCAGAGGACAAGACAACCTGTAGGTGAGTCCGTGAATGGTGTCAACAGCCGG
CCTCCTCCAGTCAGATGCCATGAAACAAGACAAGTACGTGAGTCACTAAACCAAGAAATA
GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA
AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA
CTGCAAAGGCCATAGAAAGTGAAATGAATAAAGTTAACAACCTGTGACACCAACGAAGCCG
CTTACAAAGCCAGGTATCGTATAATTTATTCAAACGTCATATCAAAGAATAACCCAGATC
TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCTTAGCTACATGCCGATGCCA
AGGATCTGGCACCAGCGCCCTTAAAGCAAAGATAGAAGAAATTGCCAAGCAAAACTTAT
ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT
GTAAGAGAAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATTGA
CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDFKEFVPTEKLLRETKVGVENVKFKKSTNVE
ISKLVKMISSWKDAINKNKRSRQAQQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHHKLDRQVLKALYDLAKESEHPPQSILHTAKAIES
EMNKNVNCDTNEAAYKARYRIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
LKQKIEETAKQNLNAQGATIERSVTDRTFCGKCKEKKVSYQLQTRSADEPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT
GGTCAGATATACTTTTCGCATGGGTCAATACCATGGTCAACCCAACCAGTTCTTCTTTGCG
TTTTCAAAGTTGTATAATATTCAAAAACGCTAACTGATAATTTGGGTGAGTTTCGAAA
GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCCAGATGTTAACTGCAGTCA
TTTTGTTTTCTTGGTCTTTACCTCGAATAGGTTTTCTTGTTTTGTATTGTTTTCTTT
TTGGACCTTATGTTTATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG
GGATCTGCCACTGGTAACCTTCAAAATAGACAAGACGAAAAAACGGTGAATAATCCGTGATA
GAAATAATACAGAAGTAGATGTTGAATTAGATTAACTGAAGATATATAATTTATTGGAA
AATACATAGAGTTTTTGTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT
CTGATTTTTTCTTTCAGCCAACCTTGGAGACGAATCTAGCTTTGACGATAACTGGAACATTT
GGAATTTCTACCTTACCCTAACCAAGATCTTACCGTAACCGGCTGCCAAAGTGTCATAACTGGA
GCAGTTTCTTTAGAAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC
CACAAATTTGTTCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTGCTTGTGGAAGTAT
CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATCTGTGGTGA
TGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT
TTACCGGCTGTACAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDQFNNTTSSSDFFSQLGDESSFDDNWNINWSTLTQDLTVTGCSVNNWSSFLRSR
FQVLVSLVFDQCPQFVQVQDWLPMSLLLVEVSHTNLTEITWMVFIHVNSVVMMLTTGHT
STTGVLVSLTDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:
1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC
GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG
AATTGAAATCTACGATACTTGATGTTGACATTATAGCACTAGTTCCCAGGAAACCCTTTC
GAAAAACACAGCAAAAACAAGAGTACTGTAAACCAATGTAACATCTGTACACCAGGGACCC
ACACATTACCAAAATCAAAATTTATTTTCTAATGCCTGTTATTTTCTTATTTTCTCT
GGCGCGTGAATAGCCCGCAGAGACGCAACAATTTTCTCGCAGTTTTTTCGCTTGTTTAA
TGCGTATTTTCCCAGATAGGTTCAAACCTTTTCATCTGTATCCCGTATATTTAAGATGGCG

TTTGCTTCTCCGTTGATTTTTTCTCTTAGTGTATTTTTTGCATTAAATCCCAGAAC
AATCATCCAACATAATCAAGAATGCCTTCCAGATTCACATAAGACTAGAAAACACAGAGGTC
ACGTCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT
TTTTTAGTGTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAATGTCAAT
CAGCTAAGTGTACTCAACATATTTCTTTGTGTTTTGATTGCGAACTTTGTATTACCATCT
CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAA
CTGAGCAAAAAGAAAGTGTGCATAGCCTTTGTCATACTTCTCCTTTATTATACCATGATA
TTCAGAACAGTCATACTGTCTACTCATTTTACGGCTATAAAAGGTAACCTTTCATTTAGAT
TATGGAAGCACTAATTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG
AGTTACCACGTTTCTTTTGTTCGATAAAAATGTCCAGTTGAAAACCTGTTTACTAACGA
TTTAAAAATTGTATTTTATTACAATATTTTTTTTGTACAGCCGGTAAAGGTCGTATCGGT
AAGCACGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT
AACATGGATAAATACCATCCAGGTTATTTCCGTAAGGTTGGTATGAGATACTTCCACAAG
CAACAAGCTCATTTCTGGAAGCCAGTCTTGAAC'TTGGACAAATTGTGGACATTGATCCCA
GAAGACAAGAGAGACCAATACTTGAAATCTGCTTCTAAGGAACTGCTCCAGTTATTGAC
ACTTTGGCAGCCGGTTACGGTAAGATCTTGGGTAAGGGTAGAATTCCAAATGTTCAGTT
ATCGTCAAAGCTAGATTTCGTCTCCAAGTTGGCTGAAGAAAAATCAGAGCTGCTGGTGGT
GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MPSRFTKTRKHRGHVSAGKGRIGKHKRHPGGRGMAGGQHHHRINMDKYHPGYFGKVGMR
YFHKQQAHFVKPVLNLDKLWTLIPEDKRDQYLKSASKETAPVIDTLAAGYGKILGKGRIPN
VPVIVKARFVSKLAEEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGTCTTTTACAATTCCTG
GGAGTTTGGCTATTGCTACCCCTGGTCTTAGCACCACCTTTTTTCCGCTATTGTATTGT
TGAACATAATTTAGTATCTATTTCCATTTTCATTATAATTCACGTTTTTAGCAGCCTCTCTT
CTTCTAGGTAATTGGAATCTTCTTCTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG
ATCTCAATATGTCCCGATAGGCCAATTTTGCCACCAGATAGTTTCGATGGCATTTTATTTT
TAGTCCTTTTGAAAGCAATATCATAAAATATATATAGTTCTCCATGATGTTCCGGTCAGT
CGCTCCGAAGCGTAACCTAGTATAATAAATAGTTTCATTGCAGAAAATAACGAAAGAAATG
GTGGAATACGATCTGTTATATCTAAACTAAAGCTAACTAACGGAATAAGCAAAATACGAAT
CGACCGCTAATTTAACAATATGGTTTATAGCAATGGAAGTAGAGTGGCACCAGGAAATTC
CTGGGCTCAATCAACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATTAT
TGAATTCCCCAAAACCTACGAAAACATTCCCTGGTTCCCAGCCTGTGTCTTTTACGATT
CTGATGTGGAAGAGAAGCTGCTTGCATGATTACTACGTTTGTGAGAAAACAGATGGTC
TGCGGGTGTGATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA
TTGATAGGGAAAATAACTATTATCTGGTTAATGGATT'TAGGTTTCCCAGATTACCCCCAAA
AGAAGAAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACCTG
TCATACAACTAACCAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTTCGATTGTC
TTGCTATCAATGGTAGATGTCTCACACAATCACCAACAAGTTCTAGACTAGCCACCTTG
GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCCTAATCGTTGTACTA
CTTTTCCGTTCAAATTTCCATGAAACATATGGATTTTCAGTTACCAATTAGTAAAAGTTG
CTAAAAGTTTAGATAAACTACCACATCTTTCTGATGGTCTGATATTTACTCCTGTGAAGG
CACCTTACACTGCCGGCGGAAAAGATTTCATTGTTATTTAAATGGAAGCCAGAACAAGAAA
ACACCGTGGACTTCAAATTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTGCCTA
AAGATGATCGGAACAGGTGGTATTACAATTAGACGTTAAGCCAGTTTTCAGCTTATATG
TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAACATTTTCGACCAGCCTTTCGATA
GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG
ATGAGGAATGGCAAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT
GCGCAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTTCAGGGATGATAAGTTAA
ATGGTAATCATACATCGGTGGTCCAGAAAGTTTGGAGAGTATCAACGATTTCAGTTTCAT
TGGAGGACCTCGAGGAAATGTTGGTGTATTTAAAGGTGCTGGGACGAGAGAAAGAGCAA
ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAATGCGACATTATCTA
CCTCTAAGCCAGTCCATTCACAGCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG
AGGATGATTGGTCCGATTAG

YGL130W, 459 aa (SEQ ID NO 102)

MVLAMESRVAPEIPGLIQPGNVTQDLKMMVCKLLNSPKPTKTFPGSQPVSFQHSDVEEKL

LAHDYVCEKTDGLRVLMFIVINPVTGEQGC FMIDRENNYYLVNGFRFPRLPQKKKEELL
ETLQDGTLLDGE LVIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP
YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLS DGLIFTPVKAPYTAGG
KDSL LLLKWKPEQENTVDFKLILDIPMVEDPSLPKDDRN R WYNYDVKPVFSLYVWQGGAD
VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET
GAWEMLRFRDDK LNGNHTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG
RPLPSQSQNATLSTSKPVHSQPPSNDKEPKYVDEDDWS

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)

CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT
CAAAAAGAAAGGTTTGTAAAAGAGCATTTGGGCAGAGAGTATTTGTCTGCGTATAGAGGA
GAAAAAATTGTACTGATGCTAATTTTGGTGTCTGTTCTTTTATTTTGTAAAGACTGT
TTTCCAGAAATGTTTGGGTTTATTTTAAATTTTGAACATTTTTCATCCTTTCTC
ATTTTGTCAATTCATTTTCTGTGGAAAAATTCAC TGACGCGAAGAAGCGATGAAATTC
CAACATCCTCCCATCATCCCAATATTGGCATAACACACATGCAGCACAGCGGAACTGCG
GAGGTCAGAGGCAATGTGGCAGAGACGCTGGCGCGCTGTATTGTATAATAGTATATTTT
ACACTCAATTCATTTTTTGTATTTAAATAGTGTGTAAAAGCTTCTGAAATCAAGAAG
CCCGTACCAGAAGTTCAATCATGAAATACATCCAACTGAACAACAAATCGAAGTCCCAG
AAGGTGTCAC TGTCAGCATCAAGTCCAGAATCGTCAAGGTTGTTGGTCCAAGAGGTACTT
TGACCAAGAAGCTTGAAGCACATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTACACACGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCCTCAAGTCTT
TGGTTGACAACATGATCACTGGTGTCCCAAGGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCCAAATTCATTGAAG
TCAGAACTTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTACTA
TCGAATTTTCCACCAACGTTAAGGACGAAATGTCTTGTGTCAGGTAACCTGTGCGAAGACG
TTTCCCAAACGCTGCTGACTTGCAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTA
AATTTTGGACGGTATCTACGTTTCTCACAAGGGTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)

MKYIQTEQQIEVPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFTKVNQLIKVAVHNG
GRKHVAALRTVKSLVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD
KKIRNVFVRDGV TIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVRNKDIRKFLDGIY
VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)

AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCTTTCAT
CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT
CAGGGAAGTCATATGGGATGGTGTCTTCTACATCTCTCTCCAATCGTGTCTTCAGTTTCC
AAAAC TCGGAATACCTTTTGTAAAGGCGCTTGTGTTGGTGTACTAACACCGTATAAAACAT
ACTTGGGGTTGATTTTAACATCGTCCACCTTGATTCTTAAC TTTTCACTCATTTTCCCTA
CAGAATTAGCTGCCATCAATATCAATTATCAACCTTATATGACTTTATTGTTTTTGT
TTGTTGGCTAATTAATTGATACAAATCTTTAGGCGAAAAATAAAAAAATATAAGTAAA
GAAGGAAAAATTAGGCGATATTA AAAACAAATCTAAAAATAAGACAAGAAACGAAAAAGAG
GTTAATCAAGTATTGGAAAAATGTCCAAAGTGTTTATTGCCACAGCAAATGCAGGTAAAG
CTCATGACGCTGATATTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTACG
GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTAGATAATGAAAATCCAAAAGATA
AGTCATATTTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTGCGATGTCTTGCAAGCTA
TTGAGAGAGATGCATTTGAATTATGCCTTGTGCTACCACTTCATTTTCTGGCGATTTAC
TCTTCTATCGTATCACTAGAGAAGATGAGACTAAAAAAGTTATATTGAGAAATTTGGATC
TTCTAGACTCAGACATGAAAAAGCATTCCTTTTGGGCATTAAATGGGGTGCCTCAAATG
ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA
AGTTTCAACCGTTTGCAGATGAGTCAAATCTTTAACACTAAATTGGAGCCCCACGTTAG
AATTACAAGGCACTGTGCAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA
TCTCTGAACGAGGACTAATTGCCACAGGTTTAAATAATGGAACAGTACAAATTTCAGAAC
TATCTACATTACGCCC GTTGACAATTTTGAATCTCAGCATTCATGATTAATAATTCGA
ATTCCATCAGATCGGTGAAATTTTCTCTCAAGGATCCTTATTAGCCATTGCTCAGCAT
CAAATTCATTTGGTTGCATCACTCTATATGAACTGAATTTGGTGAAAGAATAGCTCCT
TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTCTAGCTGGG
TCATGAGTCTATCGTTTAAATGATTCTGGTGAAACATTATGCAGTGCCGGATGGGATGGTA
AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

ATGATATTGAAATTGAAGAGGATATCTTAGCTGTTGATGAACATGGAGATTCTTTAGCTG
AACCTGGTGTCTTTGACGTGAAGTTTTTTGAAAAAAGGTTGGAGATCTGGTATGGGAGCTG
ATTTAAATGAAAGTTTATGCTGTGTTTGTTTAGATAGAAGCATCAGGTGGTTTAGAGAAG
CTGGCGGTAAATAA

YGL213C, 397 aa (SEQ ID NO 106)

MSKVFATANAGKAHDADIFSVSACNSFTVSCSGDGYLKVWDNKLDDNENPKDKSYSHFV
HKSGLHHVDVLQAIERDAFELCLVATTSFSGDLLFYRITREDETKKVIFEKLDLLSDMK
KHSFWALKWGASNDRLLSHRLVATDVKGTTYIWKFHFPFADESNSLTNLNWSPTLELQGTVE
SEMTPSQFATSVDISERGLIATGFNNGTVQISELSTLRPLYNFESQHSMINNSNSIRSVK
FSPQGSLLAIAHDSNSFCITLYETEFGERIGSLSVPTHSSQASLGEFAHSSWMSLSFN
DSGETLCSAGWDGKLRFWDVKTKERITTLNMHCDDIEIEEDILAVDEHGDSLAEPGVFVDV
KFLKKGWRSGMGADLNLNESCCLDRSIRWFRFAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107)

CTGGTTCCAACCATATCTTATGGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA
TGGAGGGACAATAGCGGGGGCCTTTGATGGTCGTGTCTGAATATGAATGGATTGATGCA
AGTTATTGCGCAAAAAGTCGTGCATTTGAGGTGTGGTATGTGTGCCAAAGCAATCCAGTT
GCTTCGTGGGTTCGACTGACACGGTTTCATTCAGAAACTCATAGGGACAGGCAACGCAT
CTCCCCTTCGGACCTCCAGAGCGCTGAAATCAATGGATTCTTGGCCAGCCTAGCCGGAG
TGCCCTGTTTTCAAACGCCCTAACTGAAAGCCACCTCATTTTGTAGAGTATTGCTGATCC
CATATGTTGGCTGCTCGCCAATTCTCTCTGCTGCAATACGCTTGTCGCCCGATGTGAATTT
CTGCACTGAGAAACGTACCTGTAGTGATTATGACCTGATCTGCCCCAACCTGGGTACCGT
CATCCAGAACCACACCTTTGATGACCTTGTGGCCACATCCGGGGTCATACAAGATCAAGT
CAGCAACTTTGTCTTGCAGCAGAGACAAAGTTGGGGTGTGCTTTCTTGTCCGAAAGTTCCC
TTTGCATGTATTTCTTATATAACTCTCTGTCTATCTGGGCTCTGGGCCCCCACACAGCAG
GACCTTGCTTCTGTTTTCAGCATTTTGAATTGCACTCCAGCGAGATCAGTTACTTTGCCCCA
TCAGCCCTTCGAGAGCGTCGATTTCCCTTTACAAGGATGCCCTTACCCACTCCACCAATAG
AGGGGTGTCACGAACACTTACCAATATCTGTTAACGATGGTGTAATGAGAGTAGTATGCG
CACCAGTCCTAGATGACGCAGCTGCAGCTTCGCAGCCTGCATGTCCAGCACCAGTACCA
CGACCTGTGTCTTGGTTGTGGGTGGAAGCTTGTCAAAGAAGATATGGTCAACCGCCTCC
TGAGGACCTGTAAGGGAAATGAAGTACACGAAGACGCCAAGGTTGTTACACGCAGCATCG
TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108)

MTLWPHPGSYKIKSATLFCSRDKLGCAFLSESSLCMYFLYNSLSIHALGPHTAGPLLLFS
ILNCTPARSVTLPIPSRASISFTRMPLTPPIEGLHEHLPISVNDGVMRVVCAVLDDA
AAASQPACAPMTTTCVLVVGWKLKEDMVNRLRLRTCKGNEVHEDAKVVTRSIVLWGV

YGL260W, 731 bp, CDS: 501-731 (SEQ ID NO 109)

TACCATGGAACACCGGTGATCATTTCTGGTCACCTGGTCTGGGGCAATACCAGTCAACATG
TGGTGAAAGTCACCGTAGTTGAAAACGGCTTCAGCAACTTCAACTGGGTAGGTTTCCGTT
GGGTGGGCGGCTTGGAACATGTAGTATTGAGCCAAGTGAGCTCTGATATCAGAGACGTAG
ACACCTAATTCAACCAAATTGACTCTTTCGTGCACTGAGCTAGAGTGGTGGTTGCGGAA
GCAGTAGCAGCGATGGCAGCGACACCAGCGCGATTGAAGTTAATTTGACCATTGTATTT
GTTTTGTTTTTTAGTGCTGGTATAAGCTTAACAGGAAAGAAAGAAATAAAGATATATTCT
CAAAAGCATACAGTTGAAGCAGCTCTATTTATACCCGTTCTCTATCAGTCATCACTACT
TAAACGATTCGTTAACAGATGCTCATTTAGCACCTCACATATCCTCCATATCTCATCTTT
CACACAATCTCATTATCACTATGGAGATGCTCTGTTTTCTGAACGAATCATACATCTTTC
ATAGACTTCGTATGTGGAGTATTGTATTATGGCACTCATGTGTATTTCGTATCGCGAGAAT
GTGGGAATGCCAATTATAGGGTGCCGAGGTGCCTTATAAAACCCTTTTCTGTGCCTGTGA
CATTTCTTTTTTCGGTCAAAAAGAATATCCGAATTTTAGATTTGGACCTCGTACAGAAG
CTTATTGTAA

YGL260W, 76 aa (SEQ ID NO 110)

MEMLLFLNESYIFHRLRMWSIVLWHSCVFVCAECGNANYRVPRCLIKPFSVPVTFPFSVK
KNIRILDLPRTAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCTAAATATGTACTCTTTTATTT

TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCCCT
GTGTAGCCTAATGTTTAATGCCTAATTTTTTCTAAAATGCAGCAACATACATATGTTGA
GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACA
TTTTAAACATCCGTACAACGAGAACCATACATTACTTTTTTTAATATTCTTTTGT
CACCGCCTTCTTTTTATTTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA
GCTAGGATACCAAATTGAAACTTGGACATACTCATCATTAAAGAAGTATAGTGTAAAGA
GAGGCATTCAATTCGTGTATTATAACGTTTAGCATCAGTTACCCCTTGAAAGCCCAACATA
TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCAAAACCCTATGCGTGATTTGAAGA
TCGAGAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCT
CCAAGGTTTTAGAACAAATTATCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTCGGTTTTCGGTATTGACGAACACATTGAGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTCTATGTGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA
AATAA

YGR085C, 174 aa (SEQ ID NO 112)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRVTFGIR
RNEKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKCKGTGVSNSHKTTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:
886-1258 (SEQ ID NO 113)

AGCCATGTCGGTCGCACTAGACTTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT
CCTTTTTTTTTTGGCATTCTTATACATTTCTTTCTTCTGAAATTAACCTGTACACCCA
TACCTTATATACACCCATACCCATATTTTAAATATAAAAAAGTAACTTCATTTTGAAAGA
CCACTCTGCATCAGCACGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCCT
TTCAGAAGGTCTGCTCTTGTGGCTGGTTCATGGGAGACACCCAGCGGAGCTCCTCCCGAG
AAAGGCCCTTCATCTCTGCCGATTGCTGACGGAAGCAGTAGCGGAGGTTTGAGTTCTC
TACGCCGAGAGTACACTGCCGTAATATCACAAATGTTTCGACTAACGGTTACAGTACGTTA
AATTAGATACTGCCATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG
ACAACAGGAAATAAACAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAACCTCTGCTAGAA
AGCTACGTGTCCACAGAAGAAACAAGTATGTTGACTATTTCAAATTAATAAAAAACCTATC
AACCCCTATTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA
TTTATCAAGTAACATATCCTGGCGCAAATCAGTTTGGAGAGGCTTAAATGACACGTCAC
AGTGATAAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCAATCTATAGT
GTGGAATAAAACCTTTTCTTCCCAAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTA
CAACGGAATCATTTTTTTACTAACAGTTTTTTTTTATTATTATAGCCGTTGGGCCGAAAA
CAACTACAAGAAGAGATTGTTGGGTACTGCCTCAAGTCTTCTCCATTGCTGGTCTTCTC
TCATGCCAAGGTTATCGTCTTGGAAAAATTTGGGTATCGAATCCAAGCAACCTAACTCTGC
TATCAGAAAGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCACTGCTTTCTGT
TCCAAACGATGGTTGTTTGAACTTTGTGACGAAAAATGATGAAGTCTTGCTAGCAGGTTT
CGGTAGAAAGGTTAAAGCTAAGGGTGATATCCAGGTGTTAGATTCAAGGTCGTTAAGGT
CTCTGGTGTCTCCTTGTGGCTTTGTGGAAGAAAAAGGAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114)

MGKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFAKSSPFGGSSHAKGIVLEKLGIE
SKQPNSAIRKCVRVQLIKNGKKVTAFPNDGCLNFVDENDEVLLAGFGRKGKAKGDIPGV
RFKVVKVSGVSLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)

GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT
GTATGTACTGTGCATCGTCATGTAGCACTATTTACGCCGTATTTTTCTTTTTTCTTTTCG
CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTCTAGAAAGTTCCGGAAATTCG
GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTTCTTGTTCGGCGATATTTCCGAACCA
GGTCGGGTTGGGCTAACAGCCGCCAGGATGGAAGAATTAAGAATTTATAGAAGCCTTC
AGTTCTTGGCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA
AGCATTAGAACAATCTTTTCTCATTGACAGGTATTCTCATTGCTCTATATATATTTTCTT

CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA
GACCCCATTTACAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC
TGCCATCTTTTAGTCAGCCCTACATTCGCGTTATTTTGATTGCAGTTCTCCAGTGAAGCT
ATTATCCAGAATGTAAAAGGAGGAAAGCAATAAAAGCTAACCTAAGAGCTCCAAAAA
GCGATGCAAAATTGTTTCAGAACCTTTGAGGTATGCACCTTGCTGAAACACCAAAATGTTTATA
CATTAAGCTTGTCTAAGCGGATTCCATATGAACTTTTTTCAAAGTACGTTAATGAGAAAT
TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTACCATGTTGTCCAAGATTTTTTTG
GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA
AAGATCTGGATTTTAGAGCCATAGGAAAAGAAATTGCTAAGGATCTTTTCCAAGACTACG
AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT
TTAAGGAATTTCTCTAGACCAAGTGTGTTGAAGATGTTTTGTTATTGGCTGTGGAGTTG
AAAACATAGATGATGGCTCGAGAGAAAAATATGCACTTTTAAAGATTGGTTTAGTTAAGC
ATGAAAGTATAAACAGTATTCTGATACGATCAACGAACCAAGATGCCAATAATTGAATCCA
AAATAGACGAGTCTCACGATGATGTTAACAATGCTCTGAATCTTTGAAGGAGGAAGAAGCGG
AGAAAGCGAAAGAACCCTAACCAGAAAGACCAAAATAAAAAAATGGATAGAGGAAGAAA
GATTGATGCAGGAGGAAGCAGAAAATCAGAACAGGAAAAAGCTGCCAAGGAAGATGAAG
AAAGGCCAAAAGAAAGAGAAGGAAGCCAGATTGAAGGCAAGGAAAGAATCTTTGATAAATA
AGCAAAAAACCAAGAGGTCCAGCAAAAAAATTGCAAAATTCAAATCATTGCCTATCT
CTGAGATTGAGGCCAGCAATAAAAAATAAATAGCAATTCTGGTTCAGCAGAAAGTGATA
ATGAAAGTATAAACAGTATTCTGATACGATTTGGATTCTCTGTGTCTGGTAAATACAC
TAAAAAACACGCTTCACCCCTATTAGAAAGACGTTGAGGATGAGGAAGTTGACAGATACA
ACGAGTCCCTAAGCAGATCTCCAAGGGAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)

MFSIFNSPCVFEQLPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKKS DANCSE
PLRYALAETPNGYTL SLSKRIPYELFSKYVNEKL GELKENHYRPTYHVVDFFGNQYYVE
DEADEDALLRSALKDLDFRAIGKKIAKDLFQDYEIELNHRGDELSILSKKDKIFKEFSLD
QVFEDV FVIGCGVENID DGSREKYALLKIGLVKHEEEISEGGINEPKMPIIESKIDESH
DVNMSESLKEEEAEKAKEPLTKEDQIKK WIEERLMQEESRKSEQEKAKEDEERQKKEK
EARLKARKESLINKQKTKRSQQKLQNSKSLPISEIEASNKNNSNSGSAESDNESINSD
SDTTLDFSVSGNTLKKHASPLLEDVEDEEVDRYNESLSRSPKGN SIIIEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)

CAAAAAGTTTTTCGGATGAACCGGATTAATACAAGTAAAATCAGCAAAGATATAGAAGAC
AAAATAAGCGTGAAAACAATCATAAACCACTCACAAACGGGGTTTTTCAGCTGTTACTCCT
CCATACATACATTTTGATAAAGATATAATGTTATATTTCTTTTCGTAATTTTGTTTTACT
TCGGTTTGCTCTATAGATTTTCATCAGCCGCACCGAAAAGGGAGATCAATAAGGTACCCTT
TAAAAGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTGGATGA
AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT
CTTCTTCATATAAATTGAAC TGCCAAATCTCTTTCACATTATCCAGGATAGTTTGGAATG
TGTGTTACTGAAGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA
TTCAAACAAAGTTTACTGAAATGAAGTTAGATTGAGGAATATACTCAGAGGCACAAAAGAG
TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC
CGACCGCATACATGAGGAGAGGCTATACGGTTCCTGCACATAGCTTAGACAACATCAACG
GCGTAGACACAAC TAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG
GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTTGATGTTCTCTCTCA
ATCATGTAAGGGAATTTGTA CTGGTTCCCTGCATTTATGTTCTTTGCATTTTGTTTTCG
CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)

MKLDSGIYSEAQRVVRTPKFRYIMLGLVGAAVVP TAYMRRGYTVPAHSLDNINGVDTTKA
SVMGTEQRAAMTKGKSLQEMMDDEVTYLMFLFNHVREFVLGSLHLCSLHFVFAFNHSTT
NNEGDCDFT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)

AATCTTTGCGATTGAATTGCTGCACGAACATTAAACATTAGTTCTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATCTGTTTTGTTTCAGAGTAAAATCCACAACATTTTTACAAATTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCTCTGTAAGTTGTCCATTGTTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCAGTTTTCTCTCTGAAATTTAA

TGCTTTCATCCTGTATGGTAGCGGTAGACATGCTGGTTTGTAGCCTTTTATTTCCTTTTT
AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAATATAATTTTCAAGAGTACG
TAATGGAAAAAGATAAAAAATAAGGACCGTCATAAAAAGAGACGTGATTAAACCTAAAAAT
CTAAAGTAAAGAAGTGTAAGATGGTTGAGGAAAATTCCAGAGTTTGTATTGTTCTTCCTT
ATACACCGCCTAGTGCTACTTTGCAGAGGATTATAGGGCAAACCTATTCCGTTCTTAAGAG
AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAACCTCATTCAGTTGG
ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCCTTTTGGGCTATGGAATGA
TCAACAGCGGAATCAACATCATATTCAACAATATTCATTTTCGTCGAGAGTAATTTGCAAT
GGAAAGTGGTTTTATTGCCACAGGAATCCACTTTTGAAACTTGGAAGCTAGAGTTGGGAC
AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAAGAGATAG
AAGGTCCCAAAGATGCTAACAAATTTTCATGTCACCGCATTTGGGCGGAACGTTCCGACCACA
TTTCAGGATGGACATAAAATATTGTTGAGCGTCTCTACATTCATCACGTCACAAAGGTTAA
TTTGTGGAATTACGTGCGATGAGCTCTTGCAAAAACAAGAAATACAAAGAGTTGATTGAAC
CTTATGATACACGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAAAACCGGATCTCT
CCGTAGAAGTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG
AATGTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA
TTGAAAAAGGCATGAGCCATTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG
AAGACGGCTGGAGCGAGAAGTTAAGCAGCACGGAAATCAGACGCCTACTTAAGTCCTCTG
CTTCGCCAACGTGCACTCCACAAAACCTTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)

MVEENSRVLIVLPYTPPSATLQRIIGQTIPFLRECQSQLDIVIVPEFKTSFOLDSALGKM
YSITRDVLLGYGMINSGINI IFNNIHFVESNLQWKVLLPQESTFETWKLELGQGQYHSI
EHYALHDNIMEEIEGPKDANKFHVLTALGGTFDHIHDGHKILLSVSTFITSQRLICGITCD
ELLQNKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPETCLVVS
ETVSGAETVNKTRIEKMSPLAVHVNVNLGGREEDGWSEKLSSTEIRLLKSSASPTCTP
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)

AGAGAGCCATCCGTAAGCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA
CCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAGTGT
CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTGAAGGAATCTG
CAAAGACTATTGTCGATTCTGGCAAACCTACCATCCAGCTTGTGTCTACTTTCGTGTGAA
TACCGTAAGAAATGGAATAGAATATATACGAATGTATACGAATATTATAGAGAACGTTCT
CTTTTATTTCTATAATGAATAGGTTTCGGGTAACGGTTCCCTTTTTTAGGTATTCTAGAAG
ATGAGAGAAGAGGGAATAATGAGAAAGGCGAAAAATAAAGGACACCTTTAACGAAAAGATC
AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAAGTGAAAAC
AAAAGTGAAGGATAGATCAATGTCTTACAGAGGACCTATTGGAAATTTTGGCGGTATGC
CAATGTCATCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAACC
AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCCTTTTGAAGTTTGCCTCCAGAA
TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATGAAGCCTTACATTCCAAGTTTGT
CAAGATTTTCTATTGTGGCCACCTTTTATAGAAGATTCGTTTAGGATCTTATACAATGGT
CAGATCAAATTTTTTATCTGAATAAGTGGAAGCATTACCCATACCTCTTGTCTGTGT
TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTAGTTTTAAGAAAGC
AAACCAATTATGCCACCGGTGTGTTATGTGCTTTCGCTTATTTCTCAAGCATTAGTTTATG
GGTTGTTTACGGGTTTCATCATTTGTCTTAAGAACTTTAGTGTTATTGGTGGGTGTTTAA
TTGCATTTCAGCGATTCAATTGTTCAAAAACAAGACAACATTCGGGTATGCTTCCTGAATTA
ACAGCAAAAACGACAAAGCGAAGGGTTACCTGTTGTTTGCTGGTAGAATTTAATTGTTT
TAATGTTTATCGCTTTCACTTTTCAGTAAATCATGTTTACTGTTGTTTGGACCATATCG
GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA
TACTAACTTTTTACAATATCACGCTAAACAACCTACTGGTTTTATAACAATACTAAGAGAG
ATTTCTTGAAGTATGAGTTTTACCAGAACTTAAGCATCATTTGGTGGGCTTCTATTAGTTA
CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFGMPMSSSQGPYSGGAQFRSNQNSTSGILKQWKHSFEKFASRIEGLTDN
AVVYKLPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHPYFFVVFVFLVVVTV
SMLIGASLLVLRKQTNATGVLCAVISQALVYGLFTGSSFVLRNFSVIGGLLIAFSDSI
VQNKTTFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNITLNNYWFYNNTKRDFLKYEFYQNLIIIGLLLVNTGAGE

ATTCATATTCATTGAGCTATACGAGGCAGTGGGAAGGGTTATCAAAAAGTTGTAATTTAAA
AGAAAAAAGCATCAATAGCCACCAAAATAAGATGGTGAAAGTTCCGCGATATATTTGCTAA
GACCATAGGCACATGTACGCAGGCGACCAGGGCCPTTTATTTACTGTAGTTCTTTCCATG
CCCTATTAAAAATTCGTGGGCCTATGATAATTTTCTCTCCCTAGTATTGAAGAACAAAA
TTGAGAATTCGCCAACTTTAAGAAGGGTTCACATTTACTAACTATTTCTTTTCTTCTCCT
TTTTTTACACAGCTGTCGTTGTCCGTGGTTCGTTACGCCGGTAAGAAGGTTGTTATCGTTA
AACCACATGATGAAGGTTCCAAGTCTCACCCATTTGGTCAAGCTTTGGTTGCCGGTATTG
AAAGATACCCATTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA
AGATCAAGCCTTTTCATCAAGGTCGTCAACTACAACATTTATTGCCAACCAGATACACTT
TAGATGTTGAAGCTTTCAAATCCGTTGTTTCTACTGAAACTTTTGAACAACCTTCCCAAC
GTGAAGAAGCTAAGAAAGTCGTCAAGAAGGCTTTTGAAGAAGACACCAAGCTGGTAAGA
ACCAATGGTTCCTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFHALVAGIERYPLKVTKKHGAK
KVAKRTKIKPFIKVVNYNHLLPTRYTLDEAFKSVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:
1054-1299 (SEQ ID NO 127)

TTACTTACGTCATTATATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGAT
TTAGCCCATACATTTTCAACCATGCACCATTTGGATTATAAAGAAAAAAATTTAATAAAAA
TCTGCCGGGGAAATTTGAGAAGAAAAAGGAAGGTGTGTTTCGCATTTAACACGGGCCACC
ATAAATTTTGTGTTGCCACCCATCTAGACGGGATCCGCCCCGCCAAGGCTCTCTTCCTC
TAGCTAGGCAATGTGGCTCTCGGAAAGGAACTCCCAACAGGACGTGGTGGGAAATGCAG
CAATTCCTCTCTGCTTCCCGCTGACCTTTCTTGGGCCCAGTTTAGTAAGTATGCTCTCAT
CTTTCATGTGTGCTGTAACCTTGCAAGTCATTAACACTATCTATAATTGATATTAGACGTT
AAAAGTTCTATATAGCATTTGCTTTTATTTAGAGAATACGAAAACACACCAGATAATTAG
TGCATATATATTAGATCAATATGGTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA
AACAGAAGAGAACAATATTTGAGGAATGAATTCGGATGAAATCTAGTAGAAGAAAAAAG
CCTAAAATAAAAAAGAAAGAAAGGAAAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG
AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAAACTGGTAACGGAGACTTTAAAG
ACGTGCAAGAAAGCAATTAATTTTATAGATAGGGAATTGAAAGGCTCTGTATAGCAGAAA
ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTGAGTTATGGGTAATCTAACAATAA
TAGAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGATACTGCTGGGTAATGAT
TTATCCTTCTTTTTTTGGAGCACAAATGCTCACTTTTCTGTCTCCTCTCAATCTTTCTG
ATGTATCCTACCCAACCTACAGTTTTCAAATTACTAACATCAATTTTTTTGTGAAACGA
CTTTCGTTTTCTGTTTTCTATTTATTTTATTACAGTTTTTAGTTCAAGATTTGTTGCACCCA
ACTGCTGCTTCTGAAGCCAGAAAGCACAAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC
TACTTCTTGGATGTCAAATGCCCAGGTTGTTTGAACATCACCAGTGTTTTTTCTCATGCT
CAAATGCTGTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG
GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAASEARKHKLKTLVQGPSYFLDVKCPGCLNITTVFSHAQTAVTCESCS
TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:
946-1262 (SEQ ID NO 129)

TAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA
TGTTGCTACATATTATTTTCCATAGCATTTCTCTGTACAAACTTCAAAATAAAAGACAGT
GACATCCGAACATCCGATACACCCATACATCATGAAAATAAATCCTGACATTGGAAGAAG
TCTTGATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCGCTGCATCGTACCA
ACAGTGCGTATGTTTCAGACGGAGAGACGACCTCTAGAGAGACGTCCGTCGGTGCGGCAAC
GCTGACGGTTTAGTTGTTTCGACGGGATGATGGGTTCCGCCAGGGGGAGGGAAGGCTTTCC
ACCAAGAGAGGTAATAATTATTCGTCGAAATGAACTCAGAGATACATCCATATTGTTGACA
ATGATATATCTTAATTGATGTGGTATTTTCACTGTTTTAACGTAAATTGAAGGAGATTAAAG
CAAAAAACAAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAACATGTTTAT
TTATCTCCATTAGGGCGTGAGAGTGAATTAGTACACAGGTACTACTAGAATGCTAAAGA
ACTTTTTAAATATCCTGAATCGTAGGGCAAATCCATGTCAAGCAAGAACTAATAGTTA

TTAAACTTCATTTACTTTTGGAGCTAGTTAAATATTTTCATCATTTCTAAAGTACTGAAC
ACCTGAATGATACTTTTATTGGCCCTTTTAATAAGAACTCTGGTTAGAAAATATATTGAG
GATATCATTAGTAATACTCATTAGATATTTGTGAATTTAGCCGTTTCCCCATTACAGAAA
AAAGATACAACATAATACATGTGCAGTCAAATTACTTTTTTTTAAGATCAATTACTAAC
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAGTTAACGTCCCAAAGA
CCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACACAAGGTTACTC
AATACAAAAGCTGGTAAGGCTTCTTGTTCGCTCAAGGTAAGAGACGTTATGACCGTAAAC
AATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTCCACAAGAAAGCTAAGACTACCAAGA
AGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACTAGAGCCCAATTAACCTTGAAGA
GATGTAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGCTTTGCAATTC
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK
KAKTTKKVVLRLCVRKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTCGTTTTCAATT
TCCATGGTGCACAGTATCTTAAGTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGT
TGCTCAGCCGCTTCGTGGATATTCTCTTGGACTTTTAAACATGGACCTACGTTCCGCTC
TCGAAAGACCAATATAATAAAAGTTATAAATTAACATTTTCTTATTAGGTATACGACCT
CGCGCTTCGAAGTAGAGGAGCCCTTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTACCCACGAC
GTATCAAGTTACTTCTTGGTGCAATGTCCCACTATAAAAAAATTCCTTGACGCTAGATC
GTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTCGTACAA
GGTTACTTCTTAGATGCTATATGTCCCTACGGCCTTGCTTAACACCATCCAGCATGCAAT
ACAGTGACATATATATACACACACCCACACCCACACCCACACCCACACACACCCCA
CACACACACCCACACACACCCACACCCACACCCACACCCACACACACCCACACCC
CACACACCCACACCCACACCCACACCCACACCCACACCCACACCCACACCCATCTA
ACCTGTCTCTTAACCTACCTCACATTACCTACCTCCCCACTCGTTACCCTGCCCACT
CAACCATAACCACTCCCAACCAACCATCCATCTCTACTTACTACTACCATCCACCGCCCA
TCATAACCGTTACCCTCCAATTACCCATATCCAACCTCCACTACCATTACCCTGCTATTAC
CCTACCATCCACCATGTCCTACTCACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT
AA

YHR217C, 153 aa (SEQ ID NO 132)

MSLRPCLTPSSMQYSDIYIHTPHPHPHPHPTPTHTHPHTPTPTPHPHPHPTPHPHPTPTP
TPHHTHTPHTTSLNLSLNLPSHYPTSPLVTLPHSTIPLPTTIHLSTYYYHPPPIITVTLQ
LPISNSTTITLLLPYHPPCPTHCTVVLPSILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)

TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA
CGTGCAAGCCAAGTTATAGAAAAGTACCGTGAGAGAGAAAAAAGATATAGCA
TTCAATGAGGCTTTATTGAGGGGCACGATGCTCTTTTTTTCTTCTGTACTTTATAAATAA
TTCCGTATTTCTTCGCTTTGTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG
AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGTCCTTAGAAGAACAAGGTTTGGATT
TGGTAGGGTTCTTGTACGAAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC
TAGTTTATTCGGGTAACAAGTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA
CTATGTAGTAAGTTACACAAAGCAACAAAGGATATTATTATATGTGACAGAGAAGAAATTG
CTGTAGAGATTTCATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT
CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAAAAGATTCTA
AACAAGAAACATCCGAAGAGGAAGATACTGCCGGAAGCATGAACAAAGGGAAACACTGT
CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTCGCTCACAGACTACAA
GCGTTTCATCAAGCCACCCAAAATAACCTGAATGCAAAGGAATCCGAAGACCTGGCCCAT
AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCCGGACGATGTTT
CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTTTCGTATCATCATCAT
CACCAATGTACGTAATGTTGATATCCAAAACCATCAACCTTTTTTCGAGAGACCAACTC
GAGCGATGTTGAAAGAACC AAAAGGAAACCTGTTGATGATTTTCATAGAAGAAGAGGTT
TGGGAGCTGTTGAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATACAACAGAAC
CAGAAAATGTGGAAGAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG

GAAGCGATGATCCCACGGCACCCAACTCACCAATAAACTTGGTCGTGCGAAACTGGTTA
GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAATAACGAATCAGATTCGTGAAT
TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTTAGAGGCGGTT
CTTCACCTGTGAAAGAGACAAACAACAACCTTTCAAATATGAATCTTACCAGCACAAA
ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG
TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTGAACAAGAC
TACAGATTGCCCTGTGACAAGGGCAAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG
GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGCATGAAGCGGCGTTGC
AAGGTCATATTGAGATTGTGGAAGTGTGATAGAAAATGGTGCAGATGTAAATATCAAGT
CTATTGAAATGTTTCGGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG
TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACTATACGTAACGCTAAAGGGTTAA
CTGCGTTTGAATCTGTCGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAGATTT
TGCGTGAAATAAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA
TTCATAATGACAAATCTAAAAATGGCAATAAATGCTCACACAATAGATCAGCCACCTTTTG
ATAATACCACAAAAGCCAAAAACGAAAAGGCCGCTGACTCACCTTCAATGGCTTCCAATA
TTGATGAGAAAGCTCCGGAAGAGGAATTTCTATTGGACAGATGTTACTTCTAGAGCGGGAA
AAGAAAACTGTTTAAAGCTTCAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG
AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG
ATATTACAAGTATCTTTTGGCATTCCGATTTCCCGTAAATCAAACCTCAAGGGATAATA
AAACATCCGCTTTAATGGTAGCTGTAGGTCGTGGCCATCTTGGAACTGTTAAATGCTAT
TAGAGGCAAGTGCAGATCCAACCAAAAGAGATAAAAAAGGGTCGTACCGCTTTGTACTATG
CCAAAAACAGCATAATGGGAATAACAAACAGTGAAGAAATTCATTTGATTGAAAAATGCTA
TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATGATA
ATAATAATGAAACATATAAACATGAAAAAAGAGAGAGAAAACGCAATCACCCATATTAG
CAAGCCGAAGAAGTGCCACTCCTAGAATTGAAGACGAAGAGGACGATACGAGGATGCTCA
ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACCTTCGGATT
CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA
AACGTAAAAACAAATGCCTTGCAAGATGAAGAAAAAATTAAGTATCTCACCCTCTCTA
TGGAACCTCATTTCTCCAAAGAAGGCAAAATCTGTAGAGATAAGTAAAAATACATGAAGAAA
CGGCTGCTGAAAGAGAAGCAAGACTCAAGGAAGAGGAAGAATACAGAAAGAAAAAGATTAG
AAAAGAAAAGAAAAAAGAACAGGAAGTACTACAAAAGCTGGCCGAAGATGAGAAAAAAA
GGATCGAAGAACAGGAGAAGCAGAAAGTCTTAGAAATGGAAAGATTGGAAAAAGCTACTT
TAGAGAAAAGCAAGAAAAATGGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGGG
CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACCTCAACGATAAACTTGATT
ACAAAGAGTTTTGGCGCTATATTTTGTAGACGAAAAAAGCATAAAATTTGTGCTCG
ACTTGCAAGTAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCAA
CTTCTGAGAAGATTTCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTGAAAT
TCATTTTCTGTATGGAGGTAGTTATGATGATAAAAAGAACAACATGGAAAAATAAAGAT
ATGTTGTAACTTTGATGGGGTTGATTTGGACACAAAGATTGGGTATGAGCTTTTGGAGT
ACAAAAAATTTGTTAGTTTGCCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA
ACCACGCAAAAAGAAAAGAAATTGAAGGAAATATGATTCAAATATCAATAAACGAATTTG
CAGCATGGAGAAACGATAAGCTGAACAAAGCCGAGCAGCCGACGCGCAACAGCGTTCTC
TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAACACCGTATGAGCATATCCTCCGTCC
TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEEDTAGKHEQRETLSEEVSDK
FPENVASFRSQTTSVHQATQNNLNAKESEDLAHKNDASSHEGEVNGDSRPDDVPETNEKI
SQAIRAKISSSSSPNVRNVDIQNHQPF SRDQLRAMLKEPKRKTVDDFIEEGLGAVEEE
DLSDDEVLEKNTTEPENVEKDIEYSDSDKDITDDVGSDDPTAPNSPIKLGRRKLVRGDLDA
TTSSMFNNESDSELSIDDDSKNIALSSSLFRGGSSPVKETNNNLSNMNSSPAQNPKRGSV
SRSDNSNKSSHIAVSKRPKQKGIYRDSGGRTRLQIACDKGKYDVVKMIEEGGYDINDQ
DNAGNTALHEAALQGHIEIVELLIENGADVNIKSIEMFGDTPILIDASANGHLDDVVKYLLK
NGADPTIRNAKGLTAFESVDDESEFDDEEDQKILREIKRSLIAAKKWTNRAGIHNDKSK
NGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA
SKEGRLPYVGTYVENGKIDLRSFESVKCGHEDITSIFLAFGFPVNQTSRDNKT SALMV
AVGRGHLGTVKLLLEAGADPTKRDKKGRATALYAKNSIMGITNSEEIQLIENAINNYLKK
HSEDNNDDDDDDDNNNETYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF
NNDRDVKESTTSRKRLLDDNENVGTQYSLDWKKRKTNALQDEEKLKSI SPLSMEPHSPK
KAKSVEISKIHEETAEREARLKEEEYRKKRLEKKRKKEQELLQKLAEDEKKRIEEQEK

QKVLEMERLEKATLEKARKMEREKEMEEISYRRRAVRDLYPLGLKIINFNDKLDYKRFLPL
YYFVDEKNDKFVLDLQVMILLKIDIDLLSKDNQPTSEKIPVDP SHLTPLWNMLKFIFLYGG
SYDDKKNMNMENKRYVNFDFVDLDTKIGYELLEYKKFVSLPMAWIKWDNVVIENHAKRKE
IEGNMIQISINEFARWRNDKLNKAQQPTRKQSLKIPRELFPVKFQHRMSISSVLOQTSKE
PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAACCTGACTGAACCAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC
GCCCTGAGAGATTTTATTTTCTTATAAATTTTACTAAATAAGGATTTGTACTTTTGATAG
AGTTTTTTTTTTTTCTGACGTTTGTTTAGTTAATATTATATAATAGTATTTAGGAAACTA
GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTTTTTTCAATTGTTT
GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA
AAATTGTGTTTGACATCGGCGTTTAGGCTTGGTTGTTCTGTGCACACATACGCTGCTCAC
ACCAATTCATATTTCTCAGGTTAATTTGTCTCCTCTCCAACCTTCAATAACGATTTTGCGT
GAAGGTTTAATTTTCAATTATTGCAATTTTAGCAGAGAAACGCACATAAATATATATATATT
GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG
AAGACTTCGGTTTTTAAGTTTTTAGGTCAAAAACAAATTTCTACCTTCCTTCAATGAAAAAC
TGCCATTTGCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTCTGTTGCTG
CCTCTGTTAGTAAGGCGGTGGTTCGGCGAATTACAATTACTGAGAGATCATATCACCTCCG
ACTCTAGTCCGTTAACGTTCAAGTGGGAGAAAGAAATCCAGATGTAATATTTGTGTGCT
TTCATGGTGATCAGGTTTTGTTTCAACCAGAAATGCATTATATTCGTTAGACTTGGAGG
AATTGAGTGAATTTTGAACGGTCACTTCTTTTGAGAAGCCAGTTTCCAATTGAAGAACG
TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA
CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTCACAAATTCGCAGT
TAGCAGTTCTACTAAAAGATAGAAGTTTTCAAAGTTTTGCATGGCGAAATGGCGAAATGG
AAAAACAATTTGAGTTCTCTTACCGTCAGAATTAGAAGAGCTTCCAGTAGAAGAATATT
CCCCTTTGAGTGTTACCATTCTCTCTCCACAGGATTTTTTGGCGGTTTTCCGTAATGTTA
TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAATGTACATTATAAGCACATAG
ACGGCAGCGCCTCATTTCAGAAACTTTTGATATTACACCTCCATTTCGGGCAAATAGTAA
GGTTCCCATATATGTACAAAGTTACCTTGTCTGGTTTAATTGAACCTGATGCAACGTAA
ATGTGCTAGCATCATCATGTTCAGTGAAGTAAGTATATGGGACTCGAAACAAGTTATTG
AACCTTCCCAGGATTTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAAACAGATAAGGACA
CAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTCAGGCACTATTCTAGAACCTTGTT
CCGTTGTTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT
TACAGATAGTCGGGTTGTTTCATGTGGCAGCAATCAAAAAGCGCCATTATAGCATAAAATC
TGGAATCTTTAGAACATGAGAAATCTCTCTCTCTCTACATCAGAAAAAATTCCTATTGCTG
GACAGGAGCAGGAAGAAAAAAGAAAAATAATGAATCAAGTAAGGCTTTATCAGAGAATC
CTTTCACATCAGCAAATACATCAGGCTTCACTTTTCTTAAACACAACCAGCCGCTGCCA
ATAGCCTGCAGTCTCAAAGTTCTTCAACCTTTGGTGCTCCCTCATTTGGATCATCCGCAT
TTAAAATTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAAG
ACGCAACAGATCCTGCTTCTGCTAAGCCAGTATTCGGCAAACCCGCTTCGGAGCTATTG
CCAAAGAACCGTCAACATCAGAAATATGCCTTTGGCAAGCCATCTTTTGGTGCTCCCTCCT
TTGGCTCTGGAAAGTCATCTGTTGAATCGCCTGCCTCCGGATCTGCCTTTGGTAAGCCCT
CTTTTGGTACTCCTTCTTTGGCTCTGGAATTCATCTGTTGAGCCGCCTGCCTCCGGAT
CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCCCTTTGGCTCTGGAATTCATCTGCTG
AGCCGCCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTTCGGAA
CTGCATCAAGTAACGAACTAACTCTGGATCCATATTTGGAAGGCTGCATTTGGTTTCAT
CATCTTTTGCACCCGCCAACAATGAACTTTTCGGATCAAACTTTACTATTTCAAACCTA
CAGTTGACAGCCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGGCGATCAAA
GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTGGTACGAAACCTA
ACACCTCTACGAAACCAAGACCAATGCCTTTGATTTTGGGAGTTCTTCCCTTGGATCTG
GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACCTTTTAAATTCGGTACTCAGG
CTTCACCTTTCTCTTACAGTTAGGAAACAAATCACCATTTCAGTTCCCTTCACAAAAGATG
ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG
AACACGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTTGACAGATTCTACGGTTGAGC
AAACATCTTCTACTAGATTACCGAAACTCCCTCGGATGAAGATGGTGAAGTTGTCGAGG
AGGAAGCGCAAAAATCCCCCATAGGCAAGCTAACTGAAACTATAAAAAAAGTGCCAATA
TTGACATGGCTGGTTTAAAAAATCCTGTATTTGGAATCATGTCAAAGCAAAATCCGAAT
CGCCGTTTTTCAGCATTTGCAACAAATATTACCAAACCAAGCTCTACAACACCTGCTTTTT
CGTTTGGTAACCTCCACAATGAATAAAAGTAATACATCTACGGTTTACCAATGGAAGAAG

CTGATACTAAAGAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT
TTCTACCGAGCGAAAGAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC
CAAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAAGTGCTTTTG
ATACCACAGCAAACGAAGAAATTCCAAAGTCACAGGACGTGAACAATCATGAAAAAGCG
AAACAGACCCAAAAATATAGTCAACATGCTGTGGTTGATCAGGATAACAAGTCTAAAGAAA
TGAATGAAAACCTCGAAGAATAATGAAAGGAGCGGTCAACCAAATCATGGTGTTCCAAAGGAG
ATGGAATAGCATTGAAAAAGACAATGAAAAAGAGAATTTTGATTCAAAATATGGCAATAA
AGCAATTCGAAGACCACCAATCTTCAGAAGAGGACGCGAGCGAAAAAGACAGTAGACAAA
GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACTCAACAGTGACCGGGATGAAAGTA
TATCTGAGTCCCTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG
AAGCTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGTATGTACAACTTCATTAG
AAGACAATTATGCTGAATCTGGCATAACAGACAGACCTTTCAGAAAGTTCCAAGGAAAATG
AAGTTCAAACGGATGCCATACCCGTGAAACACAAACAGTACACAACTGTTAAGAAGGAAG
CAGTCGACAAATGGTCTGCAAACTGAGCTGTGTTGAAACATGTAATTTTCTGTCTCAACAT
TTGAAGGTGACGAAAATTATTTAGCAGAGCAATGCAAACCAAAGCAATTGAAAAGATATT
ACACAAGTGCAAAAGTATCAAATATTCTTTCTGTTTCAAAAATTCTACGTTAAGGTTGA
TTGAGAGTACATTTTCAGACGGTCGAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA
ATATGGATACTTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCGGT
CTATCAATAATCTGTATACTTGGAGAATACCAGAGGCTGAAATTCTATTAATATTCAGA
ATAATATCAAGTGTGAACAAATGCAATAACAAATGCTAACATTCAAGACCTGAAGGAAA
AAGTTACAGATTATGTACAGGAAAGATATTGCAACAAATAACTGAAGATGTAGCCAAACAA
AAGAGGAGTATCTGTTTTTAATGCATTTTGATGATGCTTCGAGTGGATACGTTAAAGATC
TCAGCACGCATCAATTTAGAATGCAAAAGACATTACGTCAAAGCTATTTCGATGTGTCCG
CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAATTGTTCACTGTAAAGAATA
AGAGATTGGACGATAATCCATTAGTGGCAAACTAGCTAAAGAATCTCTTGCACGTGACG
GTTTACTAAAAGAAATCAAATTATTGCGTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA
AAGGTAAGGCTTCGTCGTTTCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT
TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTCTTCA
AAAATTTGAACATGGCAAAATAG

YIL115C, 1460 aa (SEQ ID NO 136)

MSSLKDEVPTETSEDFGFKFLGQKQILPSFNEKLPFASLQNLDISNSKSLFVAASGSKAV
VGELQLLRDHITS DSTPLTFKWEKEIPDVFVCFHGDQVLVSTRNALYSLDLEELSEFRT
VTSFEKPVFQKLVNNTLVILNSVNDLSALDLRTKSTKQLAQNVTSFQVNTNSQLAVLLKD
RSFQSFARNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE
VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPYMYKVTLSGLIEPDANVNVLASSC
SSEVSIWDSKQVIEPSQDSERAVLPISSEETDKDNTNPIGVAVDVVTSGTILEPCSGVDTIE
RLPLVYILNNEGSLQIVGLFHVAIAIKSGHYSINLESLEHEKSLSPTSEKIPIAGQEQUEEK
KKNNESSKALSENPFSTANTSGFTFLKTQPAANSLQSSSTFGAPSFSGSAFKIDLPS
VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSFSGSKSS
VESPASGSFAGKPSFGTPSFGSGNSSVEPPASGSFAGKPSFGTPSFGSGNSSAEPASGS
AFGKPSFGTSAFGTASSNETNSGSIFGKAAGFSSSFAPANNELFGSNFTISKPTVDSPE
VDSTSPFPSSGDQSEDESKSDVSSSTPFGTKPNTSTKPKTNADFSGSSFGSGFSKALE
SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP
NVSGNDLTDSTVEQTSSTRLPETPSDEDGEVVEEAQKSPIGKLTETIKKSANIDMAGLK
NPVFGNVHVKAKSESPFSAFATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEADTKETS
EKGPITLKSVENPFLPAKEERTGESSKKDHNDPKDGYVSGSEISVRTSESADFDTTANEE
IPKSQDVNNHEKSETDPKYSQHAVVDHNDKSKEMNETSKNNERSGQPNHGVQGDGIALKK
DNEKENFDSNMAIKQFEDHQSSSEEDASEKDSRQSSEVKESDDNMSLNSDRDESISESYDK
LEDINTDELPHGGEAFKAREVSAADFDVQTSLEDNYAESGIQTDLSESSKENEVQTDAL
PVKHNSTQTVKKEAVDNLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTSKVS
NIPFVSQNSTRLRIESTFQTVAEFTVLMENIRNMDTFFTDQSSIPLVKRTVRSINNLYT
WRIPEAEILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYFL
MHFDDASSGYVKDLSTHQFRMQKTLRQKLFVSAKINHTEELNLIKLFQVKNKRLLDDNP
LVAKLAKESLARDGLLKEIKLLREQVSRQLLEEKGKKASSFDASSSITKDMKGFKVVEVG
LAMNTKKQIGDFFKNLNMAL

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2:
943-1321 (SEQ ID NO 137)

TCGATCAACTCTATCCAACAATTCTATAATATCCACTGTTTCATTAACGAATATTGGTCTT

TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA
TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTTCTATTT
TTGTGCTCCGTGTGATATTTTCGTGGAGCAAACAGAAAGATGCGGAACCTCTTAGCAC
TCCGCTTGACATAGGCGGAGCATATTCCTCCTATGGGATGGGTTTTGTTGTACTCTTTT
CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTTCCGGCCTCAGGAC
GGCCTTCTCCAGTTTCTAGCGAGGCATACATTCCAACCAAAGGTGTATCAAGAATATCTG
AAATTAAAGGTAGTTGAATCTCTATTTGTTGTTGTTATTACCGCTTATTATCCCATAGTT
GAGACGACCAAGATTCAAACATGCAAATGTATGCACCATATCCATTCTAAACATAGTTTT
TCGAACGTTTCAAGCTTAAAGGGACAATTTATTTTAGAACTGAATTTTTTACCCAGTGGA
TAACATCGTATCTGTAAAGTCTACAAAATTTTATCCATCAAAAATTAAACAAAGAAA
ACTGCCAAACTGAATATGAGGAACTTTCTCTCTAGGAATGACTTAGTGAATGTACAGTG
ACTTGTGGAATAATGATTAGATTTTGAGCGGGTGATGCGACTTAACAGTCTCATTCGCT
AAGAAATATCCAAATTTGTGGTTCATGCTCTCCCCAAGATATGACGATGAGAGCTCGTT
TAAATTTTGTCTTCTTCCGAACAGTTATGAAAAAACTATTACGTGTTTTTATGATATCC
TTACTAACTTGTCTATTTTTTTATAAAATTTATTTTTTAACAGTTTTGTCAAGACTTTGAC
TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA
GATTCAAGACAAGGAAGGTATCCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA
ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACTT
AGTCTTGAGATTGAGAGGTGGTATCATTTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA
CAACTGTGACAAATCTGTTTGCCGTAAGTGTATGCTAGATTGCCACCAAGAGCTACCAA
CTGTAGAAAGAGAAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTAAATGA
A

YIL148W, 128 aa (SEQ ID NO 138)

MQIFVKLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDY
NQESTLHLVLRRLGGIIEPSLKALASKYNCDSVCRKCYARLPFRATNCRKRKCGHTNQ
LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)

AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA
ACTAACAATAGCACCGATGGAGCAAAAATAACAGAAATTGGAAGTACATCTAAACGGCCA
ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTTAAAGAGAGTCCAGCAAA
GATCAAGCTTCCAACGAGTGATGTAAATTTAAACAAATGTAATTATATAAAATATGAAACAT
CTCATATTTTAAATGTCTACTAATGTCTTACAGAGGACATAAAGTGATTTATGACACAT
CCGTACTAGTATTAAGTATGAACAAATTTTGGGTTTATTTTGCCATTTTTTTTACGCGG
GTTTCTTGAGATGCGCAAACCCACCTTTTCTAACACCACTAAGAAATATCAACTTTATAGG
CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTCAACCTCACATTTTCAACGCACATTA
AGCACTTGGTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTTGATCCGTACA
ATAATATPACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAACTTGAATTTATGG
AACGAAAAGAGGCAGGCCTTAGTGGAACGATTAAAAAGAAAGCAAGAATTTAAGAAACCCC
AGGATCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCCTACCAAAAACCGTGTGAAAG
TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTGGAATATTAATGAAG
TAAGGTTATCTCAATTACAGCAGCAACCAAAACCAAGCTAGTACAACCCACATACTTTA
TGGAGAAATTTCAAACGCAAGAAGAACGAAGATAAACAAATTGCCAAGTTTGAAGCA
TGATGAATGCAAGAGTACATACGTTTCAAGTACCGATGAGAAGAAATATGTGCCGATAATCA
CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG
ACTTAAAAACGGGCTTTGCATGAGATCAAAAATCCTTTCGGTTGGGCAAACCTTTTTGCTAAAA
TTCGCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGCCACCGTAGGCCTCATTA
GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTTCTCATGTTCA
CCATAACGGGCTTTTACGACATACATAGATGTTTATATCTTCGGGAAAAAGGGTGAGAAA
GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATTTAAACCCAGAAGTACTACCAT
GGAGACCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCAATTTAGTCATGACT
TCAAATGTATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA
AAAAGACTCACAAAAATGTGGCTCTCCCATTAACATATCTTTCATAAGTGTGCGGATT
ACCATAGAGAAGTGCAATTTTCGTGGAACAAGTGCTAAAAGAATTGAATTTAAATGGTGGGT
ACGCTTGGGCGCGCTACGAAAGTGACTCTCAACCAAGCCTATATAAGGCCAAAGGGG
AAAACGGGTTTTAATATAATCAAAGGTACTCTGAAGCGCCTGTCAAGAAGAGGAGGAAAGAC
TTAAAAAGAGCTCTCACAATTTTACGAATAGTAATTTTGCCAAAGCATTTTTTCGACGAGA
AATTTTCAAGATCCAGATATGCTGGCAAACCTTAGACAATAAAAGAAGGAAAAATAGAAA
CTAAGAAATCGACAGCACTGAGCCGCAACTAGGCAAAATTTATGAGAAGGAGGGAATCCA

GCGGATTAGAAGATAAGAGCGTCGGAGAGCGACAGAAAATGAAACGAACCACAGAAAGTG
CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTTCGATCCCACTCATGGAAAAATTTCCC
AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACCTTACTCGGTAAAAAAA
AAACTGTTATAAACGATCTCTTGCATTACAAGAAGGAAAAAGTCATTCTCGCACCTTCAA
AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAACATTTCCGGAT
CCAAGGAAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140)

MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA
IEVPQSPTKNRVKVGSHNATQQGTFEGSNINEVRLSQLQQQPKPPASTTTYFMEKFQNA
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFSLNWLWKRYIPEDDLKRALH
EIKILRLGKLFKIRPPKFQEPYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH
TLDVYIFGKKGVERYYNLRLGDVIAILNPEVLPWRPSGRGNFIKSFNLRI SHDFKCI LEI
GSSRDLGWCPIVNKKTHKKCGSPINISLHKCCDYHREVQFRGTSAKRIELNGYALGAPT
KVD SQPSLYKAKGENGFNIIKGRKRLSEEEERLKKSSHNTNSNSAKAFFDEKFNQNDM
LANLDNKRRIIETKKSTALSRELKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI
QRLGFDPTHGKISQVLKSSVSGSEPKNNLLGKKKTVINDLLHYKKEKVLAPSKNEWFKK
RSHREEVWQKHFGSKETKETS DGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)

GACATTTTGA AAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG
GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG
AAATGACTTACTATGAAAAGACACCTTTGATTTCGTCAATTTTGAACAATGGTAAGACAA
ATTCGTGGTTTTACGTTAAGCATGAGATGTTACAACAGGTGGAAGTTTCAAATCGAGAG
GAATCGGGCATTTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTCTGGGAAGC
TTGCTGTATTTTCTAGCTCTGGGGGAAATGCTGGTTTAGCAGCAGCAACTGCCTGCAGAT
CGATGGCACTTAATTGCAGTGTAGTGGTTCCCTAAAACCTACAAAACCTAGAATGGTAAAGA
AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG
AATACCTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTTGAAGACACTATATG
TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA
TAGAACAATTGAAGGAAAATGATATATCCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG
TTGGTGGTGGTGGGCTATTTAGTGGCATAATTAAAGGCCTAGATAGGAATCAGCTTGCTG
AAAAAATTCGGGTCGTTGCTGTAGAAACTGCCGTTGTGACGTATTGAATAAGTCTCTCA
AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTGCAACTTCTTTGGCCTCCC
CATACATAGCATCATTCGCGTTTGAGAGTTTAAACAAGTATGGATGTAAGTCTGTAGTTT
ATACATTTGAGACGTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG
TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA
TTCTGGAACAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCGGTGGATCAT
GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHSGSKTLYVHPFDNETIWEHSTIVDEIIEQLKENDISLPRVKALVCSVGGGGLF
SGIIKGLDRNQLAEKIPVAVETAGCDVLNLSLKKGSPVTLLEKLT SVATSLASPYIASFA
FESFNKYGCKSVVLSDDQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
EDDIVIIIACGGSCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACCTCAGCATGTGCTACTCCAGTTAATGACTTGTTCGTATCGTTCATGCCATAAG
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT
CAAGAGCGTATCTAGCCAAACGGACAGCTGTCTCATATGTTTAAATATGCTGCATAGTGT
GAGTCTCTAGTTTTTACCAGCAGCCACCGCGTTCTCGAGCAAAGTGATAGATCCCATT
AGGACTCATCATTCATCTAATTTTGCTATGTTAGCTGCAACTTTCTATTTTAAATAGAACC
TTCTGGAAATTTACCCGGCGCGGCACCCGAGGAACTGGACAGCGTGTGAAAAAGTTGC
TTTTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT
CTAAAGATTAAACGTGTTACTGTTTTACTTTTTTAAAGTCCCAAGAGTAGTCTCAAGGGA
AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
CACTCTCCGTGGTCTGTACGCCCTTTCTCTGGTGGTAATATTACCTTTACAGAAATGTTTCC
ACTCTCCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACTACGGAAGTGTATTCTG
GTATTGACTTAGGTACTACTTATTCCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTCACCGATGATG

AAAGATTGATTGGTGATGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT
TCGACATTAAGAGATTGATCGGTTTGAAATATAACGACAGATCTGTTTCAAGGATATCA
AGCACTTGCCATTTAATGTGGTTAATAAAGATGGGAAGCCCGCTGTAGAAGTAAGTGTC
AAGGAGAAAAGAAGGTTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAAGATGA
AACAAATTGCCGAAGATTATTTAGGCACTAAGGTTACCCATGCTGTGCTTACTGTTCCCTG
CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA
ACGTTTTTGAGAATTGTTAATGAACCAACCGCAGCCGCAATTGCCTACGGTTTGGATAAAT
CTGATAAGGAACATCAAATTATTGTTTATGATTTGGGTGGTGGTACTTTTCGATGTCTCTC
TATTGTCTATTGAAAACGGTGTTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG
GTGGTGAAGATTTTGTACTATAAGATCGTTTCGTCAATTGATAAAAGCTTTCAAGAAGAAGC
ATGGTATTGATGTGTCTGACAACAACAAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA
AGGCTAAACGTGCCCTTGTCCAGCCAAATGTCCACCCGTATTGAAATTGACTCCTTCGTTG
ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAAACCTAGATC
TATTCAGAAGAAGACCTTGAAGCCTGTGAGAAAGGTTTTGCAAGATTCTGGTTTGAGAAAGA
AGGATGTTGATGATATCGTTTGGTTGGTGGTTCCTACTAGAATTCCAAAGGTCCAAACAAT
TGTTAGAATCATACTTTGATGGTAAGAAGGCCCTCAAGGGTATTAACCCAGATGAAGCTG
TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTGCAAGATA
TTGTTTTATTGGATGTCAACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGTCTATGA
CTCCATTAAATTAAGAGAAATACTGCTATTTCCTACAAAGAAATCCCAAATTTTCTCTACTG
CCGTTGACAACCAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA
AGGACAACAATCTATTAGGTAAGTTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG
TACCTCAAATTGAAGTCACATTTGCACTTGACGCTAATGGTATTCTGAAGGTGTCTGCCA
CAGATAAGGGAAGTGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTAGATTAA
CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT
CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAACCTACGCTCACTCTTTGAAA
ACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGACAAGGAAACCTTATTAG
ATGCTGCTAACGATGTTTTAGAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG
ACTTTGATGAAAAGTTTCAATCTTTGTCCAAGGTCGCTTATCCAATTACTTCTAAGTTGT
ACGGAGTGTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG
GTGATTATTTTGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSSNVLVRGADDVENYGTIVIGIDLGT
YSCVAVMKNKTEILANEQGNRITPSYVAFDDEERLIGDAAKNQVAANPQNTIFDIKRLI
GLKYNDRSVQDKIHLFPNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTKVTHAAVTVPAYFNDAQRQATKDAGTIAGLNVLRIVNEPTAAAIAYGLDKSDKEHQI
IVYDLGGGTFDVSLLSIENGVEVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLTRAKFEELNLDLFKKTLK
PVEKVLQDSGLEKKDVDDIVLVGGSTRIPKVQQLLESYFDGKKASKGINPDEAVAYGAAV
QAGVLSGEEGVEDIVLLDVNALTGLIETTGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNNLLGKFELTGIPAPRGVPQIEVTFALDANGILKVSATDKGTGK
SESITITNDKGRLTQEEIDRMVEEAKEKFASIDASIKAKVESRNKLENYAHSKLNQVNGDL
GEKLEEDKETLLDAANDVLEWLDNDFETAI AEDFDEKFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDDDGDYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCCGTAGTTTCTACATCATCGGCACCTCTAACTA
AAACATTGGAGGAGTGGAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT
GTTTGATACGCTTTTCCCTTGAGACTACTCTTGGGGACTTTAAAAAAGTAAAAACAGTAA
CACGTTAATCTTTAGAATTACATAGCCATATTTATATCTTCCAGAGAACCCTTTTCGTGT
CCTTTATATAAAAAAGCAACTTTTTCGACACGCTGTCCAGTTCCCTCGGGTGCCGCGCCG
GTGAAATTTCCAGAAGGTTCTATTAATAAGTAAAGTTGCAGCTAACATAGCAAAATTAGA
TGAATGATGAGTCCTAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCGGTA
AAAACCTAGAGGACTCACACTATGCAGCATATTAACATATGAGGACAGCTGTCCGTTTGG
CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA
CTGGCCAGGTGATGGCTTATGGCATGACGATACGAACAAGTCATTAACTGGAGTAGCAC
ATGCTGAGTTTATGGGGATCGATCAGATCAAGCGATGTTGGGCTCCCGAGGAGTTGTG
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCCTGTATAATGTGTGCATCTG
CTCTCAAGCAATTAGACATTGAAAGGTGGTGTTCGGTTGTGGCAACGAGAGATTGGAG

GCAACGGTACTGTCTTGTCAGTAAATCATGATACGTGTACATTAGTGCCCAAGAAACAATA
GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAGAAGCAATAATGCTGCTGA
GATACTTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG
TGTTGGATAAAAACACGTTTCCGCCTATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT
TCATTGAGACTTTTGGTGATGATTACAGGACTTGT'TTTCGGAATAAAGTTGACTTGTCCA
GTAATAGCGTCGATTGGGATTTGATTGACTCCCAAGATAATATAATCCAAGAACTGG
AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHAEFMGI
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFVCGNERFNGNGTVLS
VNHDTCTLVPKNNSAAGYESIPGILRKEATMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTECFANKVDLSSNSVDWDLIDSHQDNIIQELEEQCKMF
KFNVHKKSKV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA
GTCATCTGCCTTCTTGAGCGTGTTCAGCAACTGGCCTACCAGCGGGACGCCCTTTGGGT
AAAGTTACCAGTGTGCGCATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAAACGAACAA
GGTAAAGTGAGGCTCTGGAAATTAAACCACTACTAAATTTCCATTTATAGACAAACTTAG
ATATTAAAGCAATGTACAAATACATACACAAATATCACTGTAAAAAATTCGGAAGAA
ACTTGAATTTGAATATGATTCTGCCACTTTTCTTGCTGTCAATTTATAGTCAGAAATG
AAAAATTGTCGAGAAATTAAATATAATATATGGAAGGACATTGAGTTTAAAG
AATTTGATTAAATGTCTCTCAATATCCTCTGTAAGAGTTATCTAAATCTCACTTTACT
TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG
AATATCAAAATTTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAAGCCAGGGTCTTGT
CAGAGAATGACGGTGATGTCTCCCATCTGT'TTGAACAGAAAGGAAATATCAGTCGATG
ATATGGATATGATTTCTTTGCCACGGAATTTGACAGGCAAATGGTTTTAGGTTTACCTA
TGTTTTTCGATCTTGAAGACGAAGAAACAAATTTGATCCACTTCTTCAGTTTCCCATC
ATTATGGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAAATGAGAA
CGGGTGAAGAACTAAAGATCTTTTCATTAATCCGTTTGAATTGGTTTCTCAAATGAGAA
AAAGATACATTGCTGCTTCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA
AGTGGTTTTTATACCCAAACCACTGCCAAAGTTTTGGAGATTTGAAGACGATAAACGAT
TCCAAGATCCCCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG
CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT
ACACAAAATCTGGTTTGAAGGAAAAGGAAATATAAAAGTACCATACACCGGTGAATATT
TCGATTTAGAGGATTACAAAAACAATACATTTACCATTAAAGTAATCAGGAAAAATACGC
AAAACCCACTTTTACCTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTAAACAG
ATGTGCCTACGTTTCAAGAATTTAGGGATGATTTTGCATACATAATAGAGTTAATCCAAT
CTCATAAATTCACGAGGTTTACGAAAGCGATTATCTTATTTATTAGATAAATTTGAAT
TGTTTCAGTACCTAAACTCTAAGAAAGAAATTTTAGCTAATAAAAAATGTTCCCTACAGAG
ATTTTATAATTTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC
GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCTGAAAGGATAGTTTATC
AAGACCCGAAACGTCAAGGAAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTTCTT
CTAATGACCAACCCATTGCGATTGGGTTGAAATTGATTGATGATGAATTTCTGGATTGGT
ATAGAAATATTTACCTAATAGATTACCATCTAATCCTAACAAAGTAGCAAAGTTGGTCG
GCAAAGAAATGAGGTTTTACCTATTAGCCAAAGTGT'TTCTGGAGTTTGATAATTTTATTG
AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTTCATATCCTCGAAAAATCAA
AGTACCAATTTGGCCCAAGTATCAGTTAATTTTCAATTTCTATTCCAGTGGTGAAGACTGGT
ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA
ATATACAAATTTGCCAGGATTTTCCCAAATATTCAAGGAAATGTCGTGCAAAATTTCC
AGGAGTTTTTGGATCTTATCTTCAATCCTTTATTCACTCTGGAAAAGGAGCATTACCAA
TAGATTCATCTGTAAATACTGATATCATTGGTCTGCAGTTTTTTTTTATCAAATGTGTGTT
CTATGGATCTGGTCATTAAAGAGTCGGATGAATATTACTGGAAAGAATTTACTGATATGA
ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAAGTGTGCGCATTACATGT
ATTATATTTATAAAAGTTTAGCGAAAAGTTAATTTTCTGCGGTCAAAAATCTTCAAATA
CAATCACCCTAAGAAATTTATGTTCTCCACTATCCAGCAGAACTTCCCAATTTGGAGTGG
ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG
GTCTGTACAGGTAGAACCGCTTTGGGATCTGCAACAATGATTCAATATTTTATTTATC
TCTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGTTTCACTTGAATTCGCAAA

AATCGACCTTTTTGAAGAATAAAAAACGTGCTTCTAGAACATGATTATTTGAAAGACCAGG
AAACAGCCAAAATCAATCCTTCTAGAGATATCACTGTGGGCGAACAAGATCATATGAGA
CAAATCCTTTTCATGAAAATGTTTAAGATGGGACTAAAAATTTCTTTATCATCAAAATCGA
TTCTTTTACAATAGTTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA
GTATTTACTTGTCTGAACCCAACAGATTTGTGCGAGTTGTGCGAGAACAAGTGTGCTATCTA
GTGGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT
ACTTTGAGGAGAACGTGGGTGGGATAGATAAATTGGTACGATACAGCGAAAGATACCTCGA
TAAAGCACAAACGTTCCGATGATTAGAAGAAGATATAGAAAGGAGACATTGGATCAAGAGT
GGAACCTCGTTCGGGATCACTTTGGAGTAATTAACCTCCATTTGGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRPSELLFDEYQNSVTKPNETKNKEARVLSSENDGDVSPSVLKQKEISVDDMDMISL
PTEFDRQMVLGSPMFFDLEDEENKIDPLPSVSHHYGNGESDSFVSSYTPSNLKTGEETKD
LFINPFELVSQMRKRYIAASKQDGISNKNDEKWFLYPKPLPKFWRFEDDKRFQDPDS
DLNDDGDSGTGTGAATPHRHGYYPSTYFDHYHYTKSGLKKGKGNKVPYPTGEYFDLEDYK
KQYIYHLSNQENTQNPLSPYSSKEESLEEEFLTDVPTFQEFRRDDFAYIIELIQSHKFNEV
SRKRLSYLLDKFELFQYLSNKKELANKNVPYRDFYNSRKVDRDLSLSGCISQRQLSEYI
WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFDLDWYRNIIYLI
DYHLTPNKVAKLVGKEMRFYLLAKVLEFDFNIEGEYLAEIFIKYVIHILEKSKYQLAQV
SVNFQFYSSGEDWYKKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSINFQEFDLI
FNPLFTLEKEQLPIDSSVNTDIIQLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW
TAQGDNPVTAHYMYIYKSLAKVNFLRSQNLQNTITLRNYCSPLSSRTSQFGVDLYFTDQ
VESLVCNLLLCNGGLLQVEPLWDTATMIQYLFYLFQIPILAAPLSSVSLNSQKSTFLKN
KNVLEHDYLDQETAKINPSRDI TVGEQRSYETNPFMKMFKMGLKISLSSKSILYNSSY
TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGKAPYFEENVG
GIDNWYDTAKDTSIKHNVPMIIRRRYRKETLDQEWNFVRDHFVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTTCTGCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT
GCAGGTGCGTTTCGTTTACTTTTCTCTGCGTGTCTCGAGAACTGATAAAATACTGGTTTAGGA
AAACCGTCCACTTATGGATTTAACAAGGAGGTGAAAGGTAGGTACCATGGCAATATAGCT
AGCAACGCTACGCACTAGCTGTGTGTGCTTGCTCTCTTGTGTTTCGTCTTTCGTATATTGC
GGGTTCGCCGCGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA
GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTCCAAGAA
TTCTCTAAAACATATTCTATACTTCAAAGTTTCTAGCTTCTTGCTTTTCGGTAGTTGCCA
AACAAATATCGGCATAAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACCTAAAC
AACTTAAAACGAAAACGCTTATGCTGGAGTTTCCCAATATCAGTTCTGCTAGGATGCCTAG
TAGCCGTCAAGGCACAAACCACGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA
ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA
CCTATGCGCAGAACTACGCCGACCAATATGATTGTTCCGGGTGTCTTAACGCATTCGGATG
GCCCATATGGTGAGAACCTTGCCCTTGGTTACACAGACACGGGAGCGGTGGACGCCCTGGT
ACGGGGAGATAAGCAAGTATAATTATCAAATCCCGGATTTTCTGAATCCACGGGTCACT
TCACACAGGTGGTTTGGGAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA
CGACATGGAACAATTATATTGTGTGCTCCTACAACCCCTCCTGGAAACTACCTGGGTGAGT
TTGCAGAGGAAGTGAACCACTTATAAGCACTGTTTCTCCTCGTCTCATCCTCGTCTCTT
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCCGTGTAG
CGCAAGGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAATCGACGA
CCATAAACCCTGCCAAGACCGCTACCCCTCACTGCGTCTCTTCTACCGTAATTACTAGTA
GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT
CCTATGTCTACCTCCTCGAGTACCGTCTCTCTAGTGATGCTACTTCTCATCCACTACCACCA
CCTCATCGTTGCTACATCGTCCAGTACCCTTCTTCCGACCCTACCTCGAGCAGTCTG
CTGCTTCTTCTTCTGATCCTGCCTCAAGTTCCGCTGCCGCTTCTTCCAGCGGAGTACCG
AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGCTCCTT
TGAGTAGTACTCTTACTACTTCCACCGCAAGCTCCAGAAGTGTAACCTCCAATTCAAGTTA
ATTCTGTGTAAGTTTGCAAACACAACCTGTGTTTTCTGCTCAAACAACCTCTTCTGTAAGCG
CCTCATTATCATCTGTAGCTGCTGACGATATTCAGGGTAGCACTTCCAAGGAGGCCA
CAAGCTCAGTTTCCGAACATACTAGTATAGTAACTAGTGCAACTAATGCTGCCCAATATG
CAACGAGTCTGGGTCACTTCCAGAAGTTCTTCCGGGGCCGCTCTTCTCCTCAGCTGTGT
CGCAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACCTCAGTTA
GTAGCACAGCCCATAACCACAAAGGACACCGCCACCCTTCAAGTAACCGCCTCAGAAAGTA

TCAC TTCG GAACTGCTCAGGCTTCAAGTTCAACAGAGAAGAATATTAGTAACAGTGCCG
CCACATCGAGTAGCATT TACTCCAACAGTGCTTCTGTGTCAGGACACGGTGTAACATACG
CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA
CAAATTGCTCTAGTATCGTGAAGACCACAACCTTTAGAAAATTCGAGTACCACAACCATCA
CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACCTCCACAAGGGCAG
CTACCGCAGTAACCATAGATCCCACTTGGACCCCTACCGACAACCTCAGCTAGTCCCAACCG
ACAAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT
TACGCACAACCACCAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA
CTTCCGAGAGCGATTATTCCGATAGTCTTAGCTTCGCCATCTCCACTGCCACCACCCTG
AAAGCAATCTGATCACAAACACCATCACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA
CCTCCGCTGCTTCTTCTACAGATGAGACGGCCTTCACTAGAAACAATCTCGACATCTTGTA
GCACTTTGAACGGCGCCTCAACCCAAACAGTGAGCTAACCACATCGCTATGAAAACCA
ACACGGTGGTTCCAGCTTCTTCTTCCCTTCAACTACAACCCTTGTCTAGAAAATGATG
ACACTGCCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAACCCCGGAG
AAACATCTTCTCTCGCTAGCGATTTCGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG
TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACAACCTACCAACAGACTGTTG
CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACCTACTGGTAGCA
ACGGTCGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACCTTCCCTCGA
TCTACACTCAACTAAAAGAGGCACATCAACCACCGCAAAACTTTCTGCATACGAAGGTG
CTGCAACACCTCTTCCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG
TCGTAGCTGTTCTGTTCCGCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEFPISVLLGLVAVKAQTFPNFESDVLNEHNKFRALHVD TAPLTWSDTLATYAQNYA
DQYDCSGVLTHSDGPYGENLALGYTD TGAVDAWYGEISKYNYSNPGFSESTGHFTQV VWK
STAEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTSD
TVSTISSIMPAVAQGYTTTVSSAASSSSSLKSTTINPAKTATLTASSSTVITSSTESVGS
STVSSASSSSVTTSYATSSSTVVSSDATSSSTTTSSVATSSSTSSDPTSTAAASSSDP
ASSSAAASSSASTENAASSSSAISSSSSMV SAPLSSTLTSTASSRSVTNSVNSVKFAN
TTVFSAQTTSSVSASLSSSVAAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS
SRSSSGAVSSSAVSQSVLNSVIAVNTDVS VTSVSSTAHTTKDTATTSVTASESITSETAQ
ASSSTEKNI NSNAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPATNCSSIV
KT'TLNSSTTTITAITKST'TLATTANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS
TYGSSSTGASLDSLRTTTSISVSSNTQLVSTCTSESDYSDSPFAISTATTTESNLITN
TITASCSTNSFPTSAASSTDETAFTRTISTSCSTLNGASTQTSSELTSPMKNTNTPAS
SFPSTTTTCLNDDTAFFSIYTEVNAATIINPGETSSLASDFATSEKPNEPTSVKSTSNE
GTSSTTTTYQQT VATLYAKPSSTSLGARTTGSNGRSTTSQQDGSAMHQPTSSSIYTQLKE
GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATTCATTTCCCTAGAGGAGTTTTTATAGTCCTGCCATCTAATT
GTAGAGCAATCTTTCCCTTCTCAACATCCCCTATTTAGTGACACCTTTCCCAAACCTTCT
GTGAAGTTTTTGCTCAATCTATTTGTTTCCGTAGGAGTGTTATTCTCAATCGTGTTGTCTG
TCCCCAGTGGCTGGGCATTTAATGAGTAGAATCGGGGCAGTTTCAATCTTATGGAATTCA
CAATGAAGCATCCCTTCCTTAATGATGGCAGCATTCCGTATTCTCTTTGTAGGGTTTCG
TTTGCCCTTCAAGTGTTTTGTTCTTATTTAGCCTTTTCCCTTACCTTAATTTTTTTCTTTT
CTCTGAAGAAAATGAATGAGTTTAAAGATATAGCAATTAAGAAAGTAACAGTGAAGAAATT
TCTCAGATGAGCAGATGGGAATTAAGAAGTATCTACAGAGCTCTTACTAAATTGAATC
ATAATACATACTTACAAACATGTACAGATAGCACAAAGAAATGACAGTGAGCTTAAGAA
ACGCCAGGACACAAATTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA
AGCTTGCTGAATTGACAAAAGAAAGAACTAGAGTCTTATCCAACGGACAAAGTATGGAGAT
CTTGCGGTAAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCACATG
CCGAAACTGTTCTTCTGGATCAAAGAAAAACATTAAAGATAAAGAAGAACTATTTAGAAA
CTACTGTTGAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTAA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTTCTTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG
ATAAATCATTAACGTATTTGGATTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC
ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT
GTCTGTCCAAATATGCTAGCTGCTGATTGACCATATCCAATTGTGTCTGGCGTTTCTTA
AGCTCACTGTCAATTTCTTGTGCTATCTGTGACATGTTTGTAAAGTATGTATTATTGATTCA
ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTTCCCATCTGCTCATCTGAGAAATTTT
TTCACGTGTTACTTTTTAATTGCTATATCTTTAAACTCATTCAATTTTCTTCAGAGAAAAGA
AAAAAATTAAGGTAAAGGAAAAAGGCTAAATAAGAACAAAACACTTGAAGGCAAAACGAAAC
CCTACAAAAGAGAATACGGAATGCTGCCATCATTAAGGAAGGGATGCTTCATTGTGAATT
CCATAAGATTGAAACTGCCCCGATTCTACTCATTAATGCCAGCCACTGGGGACAGACA
ACACGATTGAGAATAACACTCCTACGGAAACAAATAGATTGAGCAAAACTTCACAGAAGT
TTTGGGAAAAGGTGTCACTAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG
ATGGCAGGACTATAAAAACTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAAGTCTC
TCTTAGCATACCTATTAAAACTGGAGTGGTTCCTTATCCAGTCTTTCCATCAAACTC
ACTCTTTGCCACTAACTTCATTAGTGGCAAGATGCATAGATTTACAAATGACAAATGAGC
CTGGCTGTGACCCTCAATTAGTTGCAAAGATTGGAGGCAACAGTGATGTTATAAAAAATC
AGTTGTTAAGATATTTAGATACCGATACTTTATTGGTCTTTTCCCCTATGAATGAGTTTG
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG
AGTTTTTACGCAACTTTTTCATCCGAGTCTAATATTCGACTACAAATTTTAGATGCCGACA
TCCATGGGTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAAATATA
TGAGCAGCTTATCACCATGGGATCTTGCAATTCTTGAAAAACTGTATTAAACCACAAAGT
CCTTCATTGCGGCGTGCTATTATTAGAAAAATAAAAAAGATACTGCGAACTTAATTCCTCG
CCTTGAAACTGATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG
TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA
AAATTCATACTGCTGCGATTGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)

MLPSLRKGC FIVNSIRLKLPRFYSLNAQPLGTDNTIENNTPTETNRLSKTSQKFWEKVSL
NRDVEKGKIALQLDGRITIKTPLNGIIVDNAKSLLAYLLKLEWSSLSLSIKTHSLPLTS
LVARCIDLQMTNEPGCDPQLVAKIGGNSDVIKNQLLRYLDTDLLVFSMPNEFEGRRLRNA
QNELYIPIIKGMEEFLRNFSSSNIRLQILDADIHGLRGNQQSDIVKNAKKYSSLSPLW
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTMDNIVRAATLETIFQVEKWGEV
EDTHDVKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)

GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAAACGGTGCTTCTAAT
GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA
AGAGGTACGTGTGCTAGTGAAATAGGTCACATGTACCAGAAAATCAAGAAATCTTAGATG
TGTGTAATCTTGCAATTTAGTTTCAAACAAGATCCTTGTATTTATATAAAACAAAGATATA
ATTTTTTAAAAAAAATTAGAAAAAGCAAAATATAATTCAGGTCCCACTTGGAAATAATGGCA
CTGTATTGATGCATTTTCTTATGCTTAGTGACGCGTTTTCGCGCGTCAGTTTCAAGTTT
TTCTTGGCTTTTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAAGGATTAAAAATGCAGTA
TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCCTTCCAG
GACAGTACGCGCAAACTATTATGGAGATATTCAAGGAAGAAGAAGAAGAGCTTTTTTCGG
CGATAGAAGGTATAATATATGCCTGTGAGGTGTATGACCCTGTACCCCGTCATTTACATA
AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTATAGAAACGCATCTTTCATATT
ATACAATACTCAATAACATTTTCAAGATATACAAGCCTATCTTTCTACTTGGCTTAGGGATC
TTGGAACGACAGGTCCATACCAACAATCTTTCAGAAAGTATTTCTCTCATGTTTGACC
GCACTGTATCTATCTTCAGGAAATGTACGATAGAGGGAGGTTTTCCACATTTGATCGCAC
GTCTTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT
TTTTTTCAAGCTACGATTATGCTTTTCGGGGTTGCATACAACCTTGTAATTTGCTGAAT
ACAGGTATGACGAAGTTCATTACATATCGAACGGCACTTACTCATTAGTTGCATCGATGA
AGATAGATCCTGCTGAAGTCATTAAGGGAACATTTTAGGCTTACAATTCCGAAATTTA
ACATATCTAATATATTAATTGAAATTTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG
TGAACCTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTTCGAGTATCT
CCGAAGGTAATCATCAGGTCTAGAAATTGGGGAGAAGTTTAATGTTTCCATTGTTGAGGA
CTGGAGATTTTGAATCTGTCGTATTGACGACGCGGGAGCTGTACATAACATTTACAGAAG
CGAAGGATGTTAAAACTAGAAATAATCAGTCTGGATGAAGTTTCTGGGTAATTCAGTGGGA
AATCTTGTCTTCAAAATTATGAGAGAAGGGCAGCAATGACAGTTCATTTATCAAAACAC
ACCTACAATTTAAGAAGGCCAACAAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG

TAGACAGAAATATTCCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAAGTCCCC
CGCCTTCAAATACTGGTTGTTTCATTACACAGGTCTAAACCCTTGCATATCCCTTTATCAT
CTGTTATTTCGTGAAGACTTTTATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG
ATAGCAGTTGTGAATCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTTCATG
ATAATGAATTTTTTAACAACCAGTCACTCATTTATTTTTCAGAACACATAGACAATAACT
CGAGAGAGGTGGTAATAACAGATGAAAAATACGATAATATCTTTGGAAAAATACCCAAGTAA
GTCCGTGGTCAAATTACTCATGGCAAAAAATTTACCCGCATCAATTACAGGTCTCTATTA
TCCAACTGCGCATGGGAAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT
TCAAAATTCGTTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA
TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA
AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG
TATCGCACTCAAACAATCAAGATGCTACTGCAAGTCCACTTTTCGTCAAGTTTCATCAGCAA
TGGATCTCAAGCATTCAATACAGAAATGTTCTCTACAATAATGCCCCAAGAGTTGACGC
AGGACGTCATCGTTCAAAATCAGACCTAATCAGTAATATTTCGTCAAAAAATATAA

YJL181W, 611 aa (SEQ ID NO 156)

MEIFKEEEEEAFSAIEGIIYACEVYDPVPRHLHKSSTKIINAAKLIIETHLSYTYILNNI
SDIQAYLSTWLRDLGTTGPYQITLSEISLMFDRTVSIFRKCTIEGGFPHLIARLYRLK
SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV
IKREHFRLTIKFNISNIIIEIFHLLDGLAFFKVNPDLSISISTASAETIFRSISEGNHGV
LELGRSLMFLRLTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSFIKTHLQFKKANFNEDNNGGLIVDRNIPTDDFTLASTNRQSPPSNTGC
SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHDNEFFNN
QSPHYFSEHIDNNSREVVITDENTIISLENTQVSRWSNYSWQKISPHQLQVSI IQLRMGN
FIVAYDSYDNLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL
RVLSFYTTDHTTEAVSHSNQDATASPLSSVSAMDLDKHSLLQKCSSTIMPQELTQDVIGSK
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)

TCTTGCAACCATCGTCCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA
CAGATGCCAACATGTGGGAGATAGGGGGCTATTGCAATTTATTAACGTCTCTAGTACTG
GTAAGCCTTTCTAACATTCTTGTGGTCACGTGATGTGTATGTTTCTTTTCTTTTATTCCTC
CGGGTGATAACGACGCGAAAAATATTTTTCATTTTCTTTTAACCATCACAAATTTGCGA
CGCGACGCGAAAAAAATGCAGAGAAAGTAAAGAATGCTGGATAAGAAATCAACAACACAG
TTGAACATTGGCGTGCCCCCTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTGT
TGTATGCGTGTGTTAACTATCCTGCACATCATCTTGCGCAGTTAGTCCAATAAAAAAGGA
TTACTACTGAACAGGTCTTACTATTTTGTATTGCGTAGTGCTGGGGAAAAAGTAAACACAC
ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC
TGGACACGGGAGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAACAGGCCGCGCAAG
ACGAGAGTGATGATTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC
CATATTCGAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCAATTAAGTAATA
CAGCTTTGTGAGAGGCTAACTCCAAATTTCTTGGGAAAAATTGAAGAAGAGGAAGAAGAGG
AGGAAGAAGGCAAGGATGAGGAAAGCGTGATTCTCGTATTAAAAGGTGGTCTCCGTTC
ATGAAAAATGAAAGTGTTACTACTCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC
CTATTTCTCTCAACAATGGAACCAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA
ATACATCCTCATCTCTTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT
CGGGCCTCGTATCTAAATGTCTATGGACACTTCGTTATAACCTGCGAAATGAGGATAC
CAGAAACACCAGTGAAAAATCACCTTAGTGGAGGGAAGAGACCATAAGCATGTCCACC
TTTCGAGTTGCAAAAAATGCATCGTCTTCTCTAAGTGTTTCCCCTTTAAATTTTGTGAAG
ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCGTCTTCGAAAGCTTTACCTT
CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATTCATG
ATCGTCACAATAACCAGACAAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT
CTCCACAAACATTGCATTCTAACAAGTTCAAAAAATCAAAAGAGCAAGGAATTCGGTTA
TTTTGAAAAATAGAGAGCTAACAAACAGTTTACAACAATTCAAAGATGATTTATACGGCA
CGGACGAGAATTTCCACCTCCAATCATAATATCAAGTCATCATTTCAACTAGAAAGAACC
CTCAACCTTATCAATTTTCGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC
CAACAAGACGAAAAATCTATTATGGGGCAACATCTCAAACACATAGAGAAAGCAGACCAT
TGTCACCTCTCTGCCATCGTGACAAACACAAGTGCAGAGACGCATTCATATCTT
CCACCGATTCTTCGCCGTAAATTTCAAAAGGCGTCTAATCTCTTCAAATAAGATTATCAG
CAAATCCAGATTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC

AGTTTTCCACGGTCTACCAGGTTACGTTTGCCCAAACAAACAAAAAGTATGCAATCAAAG
CCATTAAACCAAACAAATATAATTCCCTTGAAACGCATATTACTGGAAATTAAAATACTAA
ACGAGGTAACAAACCAAATTACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA
TCAGTTCCCTGGAAGTTTCAAATTCATACTATATTATGACAGAATTGTGCGAAAAATGGTA
ATTTGGATGGATTTTTACAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGAAGATTGGA
GAATTTGGAAAAATCATCGTGGAATTAAGCCTGGCTTTACGATTTCATCCATGATTCTTGTC
ACATTTGTGCATCTGGACTTGAAACCCGCAAACGTCATGATCACATTTGAAGGTAACCTAA
AACTAGGTGACTTTGGAATGGCTACTCATTTACCGTTGGAGGATAAAAAGTTTTGAAAATG
AAGGTGACAGAGAATATATTGCACCAGAAATCATTTCTGATTGTACGTACGATTACAAGG
CAGATATTTTTTCCCTGGGTCTGATGATTGTTGAAATTGCAGCGAACGTTGTGTACCTG
ACAATGGCAACGCATGGCATAAGTTGAGATCGGGTGATTTATCGGATGCAGGAAGATTAA
GTTCCACAGATATTCATTCTGAATCATTATTTTCAGACATTACGAAAGTAGATACAAATG
ATTTATTTGATTTTGAAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA
CTGTTCAATAACAATAGTAATATCAACAACCCTAATATGAATAATGGCAACGATAATAATA
ATGTCATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAAGTTCTAAAATTTCCCG
CATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACGATGGATGA
TAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGAGGAATGCC
TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSLDEDEEDFEMLDTENLQFMGKKMFGKQAGEDESDDFAIGGSTPTNKLKFPYPSNNKL
TRSTGTLNLSLNTALSEANSKFLGKIEEEEEEEGKDEESVDSRIKRWSPFHENESVT
TPITKRSAEKTNSPISLKQWNQWFPKNDARTENTSSSSSYSAKPNQSAFTSSGLVSKM
SMDTSLYPAKLRIPEPVKKSPLVEGRDHKHVHLSSSKNASSSLSVSPLNFVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHNRHNNQTNILSPTNSLVTNSSPQTLHS
NKFKKIKRARNVILKNRELTNLQQFKDDLYGTDENFPPIIISSSHSTRKNPQPYQFR
GRYDNDTDEEISTPTRRKSIIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL
NSKRRLLISSNKL SANPDSHLFEKFTNVHSIGKGQFSTVYQVTF AQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFNQSYIIMTELCEGNLGDGFLQ
EQVIAKKKRLEDWRIWKIIIVELSLALRFIHD SCHIVHLDLKPANVMITFEGNLKLGDFGM
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLDPDGNNAWH
KLRSGLSDAGRLSSTDIHSESLFSDITKVDTNDLFD FERDNI SGNSNNAGTSTVHNNSN
INNPNMNNNGNDNNNVNTAATKNRLILHKSSKI PAWVPKFLIDGESLERIVRWMIEPNYER
RPTANQILQTEECLYVEMTRNAGAI IQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCCCGCATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACG
ATGGATGATAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGA
GGAATGCCCTGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTT
TGGACCTAAGCCAAAATTTTTATATGATAAATGGAACAAAAACCTTGTTTTATTTACA
TACTTTTTTCCCACACGTGCTTATGGGCCGATTGTATAAATAATCCAATAACGAAAAAG
AGTGAATTGCAGTCCGGTAGTAATACCATGTAAAACCTTAGATGAGTTTATTTTAAGTA
CAGCCGCTTCAAGCATTTTTATTTTTATTTTACAGATGTAGCAGATAACAACCGTTAAAT
TATATTATATATATATATATATATATATATCAAAATACGACGTATTACATATATATTGAGAAT
AAGGGAAGGATGGAAGACAAATGACAAAAAGTTTGAAGCATAAATATGTTCTTCGCTTAG
ATGTTCACTCTTGTTCTTCTCCAGTTTCTTCTTCTTAGCGTTGTAACGGATAGTGTGTTG
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTGTCTTCTTAGCCTTAGCCATTTT
TGCTTGATTCTGAAAGACTTTTGAGCCTAATTAAAAGGGAACATATCGTGCACATACGA
AGTGTA CAATTGTAAAAAATGTTAGTAACAATGTTCAAATCATCAATATGATGCATTCA
CGGATCCAAGGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHKYVLRDLVHLGSSPVSSLSVVTDSVVGSSQSDPLWQWSVLLLSLSHFLDSERL
LSLIKRETYRAHTKCTIVKNVSNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:
893-1042 (SEQ ID NO 161)

TATTCAAGAATTATTTACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

AGTATGTGATGTATGGGCGCACAGTACCAATTTAACTTTTTTTTTTTTCATTTTTTTAGC
TTGATTTTTCAAAAACTTATGGGCGTTTATAGGCTCCGGCTCAAACCTACCACCACCACGCG
GCAGGCCGAGGCAAACAGTACGCCCTTGGCGGGGACGCCGAAGCGACTCCTTCTGTTCCAA
GCTCAATGGTCCTTGCGTTTACGCTCGCGCGTGGGCTAACTAACGCAATTCGGCTTTTGG
GCTGTCTGAGAACCGAGAATTATTCTTCGCCCTTGATAGATACTTTAAAACCTCTACTTAAT
ATACTTTCTACAATTTTTGGTACATTCATATTATACTGAAAATTCGAAAAAGACAAGCAA
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCCAGTTAGA
TGCTGAACCTGATCAATAGCAAATATAAACCACATCCATCTAAATGACCTTACCACCTAC
AATTTGGATTTGAAATAGAAGCAATGTGTAAAATATAGGGAAAGGATTAGGAGTGTAAAC
CATACTAAAATTTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAAAA
TATGGTCATAAACTGCTTATTCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT
GGTATTGCCCTTGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT
TTTTTACAATTGTACACTTCGTATGTGCACGATATGTTTCCCTTTAATTAGGCTCAAAA
GTCTTTACAGATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTTGCCACA
ATGGATCAGATTGAGAACCAACAACACTATCCGTTACAACGCTAAGAGAAGAACTGGAG
AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)

MAAQKSFRIKQKMAKAKKQNRPLPQWIRLRTNNTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)

TCTCGACAGCCCAAAAGCCGAATTGCGTTAGTTAGCCACGCGCGAGCGTAAACGCAAGG
ACCATTTGAGCTTGGAAACAGAAGGAGTCGCTTCGGCGTCCCGCCAAAGGCGTACTGTTTGC
CTCGGCTTGC CGGTGGTGGTAGTTTGGAGCCGAGCCTAAAACGCCCATAAGTTTTT
TGAAAATCAAGCTAAAAAATGAAAAAAGTTAAATTGGTACTGTGCGCCCATAC
ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAACT
CAAATATTGAGGACGCGCGATTACCAGCGGCATGTTTACTCGCTGGAAGATGTGAAATAA
TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTCT
AATCTTTAAATTGTAAGGTTTTTTAATGGCCTTTTCAGTTCTAGTATTTTTTATAAAACAA
GACCAACATACATATCCAAGATGACCAGATCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTTTAATCAGACCATCCTCCAAGGTCA
TTATCAAGTTTTTGAAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG
ATGACCACAGATCTGGTAAGATTGTTGTTCAATTGAACGGTAGATTGAACAAGTGTGGTG
TTATTTCCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAATTGT
TGCCAGCCAGACAATTTCGGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG
AAGAAGCCAGAAGAAAGCACGTTTCTGGTAAGATTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)

MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLQVMQKHGYIGFEYIDHRSGK
IVVQLNGLNKCGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTTSAGIMDHEEARKH
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)

CTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAGTAGATAGAAAAGGCGATCGCT
ATTTAAGTGTCTAGACTTTCTTAACGAGAGGTGTTCCAGCTTCTATTTTGGCTTTCTCTAT
GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG
CGTAAGAGATACGTCTACGATAGCATGTAACAGCGTATATATAATCTATATGTATTCGAT
TAATCCAACACTTCTGTTGTGTAGTCTAATGTTTCAAAAAAAGGTACGCTTCCCTGTTAT
AATCAGGTATATTTCTGTTATTCTTATAAGCTAAAAGATTAAAAATTTTCCACTTTCTCT
GAAATTTGGTTCGGTTTCGTGGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA
AGATGGGATTACTGGAAAAATAAAGGAGGAAAATCCTGCAGAACGTTGTTGTTTCAATC
GAAGGTTTCTTCATTGCAAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTCAATTGG
TTTATAATGAAGATCCCGATTTACCGATGGCACAACACCATGTGATCGGTTGGGAGTGG
ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCCAGTCTCAG
ATCGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA
ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAACCTAATCTTGGAACCTAATGGTCAAG
ATGGAAGAAATGTCTTAGAACAACAAAGAGACGTGGTTGCTAGACTAATAGAAGAAAAACA
AGGAAACGCAAAAAAGGGGTGATAAAGTCTGTATTGTCCCAAGGTTTGGTACGATAAAT
TTTTCGACCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT
GCAGAGACTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGTATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG
TGGTAACTAATTTGGTTATCAACCAAACACAGGGGAGTTAGAGACAGAATACAATAAAT
GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC
AGGACGATTCATAATGTACCTCTCGATGTCTGCGTTGAATTTAGTACGTGATTTGGTTG
AAAAGAGTATGAATCTGTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGCGGTGGATT
TTAAAATTTGGTTTTGTGTCAGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT
TTTTGAATTCCTCATATGAAATAACTCCGCTTCAATTTCTCGAACTACCGATAAAGAAAC
TACTAATACCAGACATGTTTGAAAACCGTTTAGACAAGATAACTTCAAATCCGAGTGACC
TTGTCATAGAAATTAAACCTATAGAAGGGAATCACCATTGGCCTTCAAACATTTTGGCTT
ATAATAAACTCGAACCCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT
ACATGAATTCCTGCGTTGCAATGCCTGGTACACATTCGCGCAGTTGCGTGATTTTCCCTT
ATGATGGTTATGAAGACGAAATCAATGAAGAAAATCCTCTTGGGTACCACGGCTATGTGG
CTAGGGCATTTAGTGACTTGGTTCAGAAGTTGTTTCAAACAGGATGAGCATAATGCAAA
GAAATGCTGCTTCCCCCTTCAATGTTCAAATCCACTATCGGGCACTTTAATTCGATGT
TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTATAGCCTTCTGTTAGACAGTTTAC
ATGAAGATTTGAACAGGATAATAAAGAAAGAATACACAGAAAAACCATCATTATCTCCTG
GTGATGACGTGAATGATTGGAATGTAGTCAAGAACTGGCAGACGATACTTGGGAGATGC
ATTTAAAGAGAAATTTGTTCCGTTATAACGGATTTATTTGTCGGGATGTACAAATCAACGC
TATATTGTCCCGAATGTCAAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT
TGCCGCTTCCGGTTGATACAGTGTGGGATAAACTATAAAAATTTTCCCATGAACCTCTC
CACCACCTTCTTCTGAAGTTGAGTTAAGCAAATCGTCCACTTATATGGACTTGAAGAATT
ATGTTGGTAAATGTCGGGCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA
ATCAAATCTATGTTAACTATGAGTCAACAGAGTCGAATGCTCAATTTTAACTTGCAGG
AATTGATCAAACCTGCTGATGACGTTATTTTATGAATTACCAGTAACAAATGACAATG
AAGTAATGTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT
TTGGAGTCCCTTTCTTTATTACGTTAAAAGAAGATGAATTGAATAATCCAGGTGCAATAA
GAATGAAATTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCTGAACT
CTGTAGGAAATCGAACCGATTTTGCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG
ATGTTGAATTTGAACAATATAAAGATATACTACAGTATACGCTCTATTAAGGTGACTGACA
AGGATAAAATCCTTTTTTTCCATCAAGATTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA
GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCAGTTAAACCTTGACAAAG
CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCATCCT
TAGTAGATTGTGCTGAAGGGTCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA
GTGAAGCAAAGAATTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAAATAAGAAA
CTGTAAACAAATAATGAAAATGTAATAATACTAATGATCGGGATGAAGATATGGAATAA
CAGATGATGTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGAGCGT
TAGATAAAATTAAGGATAGCTTGACTTCCACTCCGTTTGCGATTCTTTCTATGAATGATA
TTATTGTTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT
ATAACTGGGAAAATCCAGCTACTTTGCCTAACAAAGAGTTGGAGAACGCTAAGTTGGAAA
GATCTAACGCTAAGGAAGAACCATAACCTTGGACGATTGTCTCCAATTATTTCCAAAC
CAGAAATACTAGGATTAACCGATTTCGTGGTACTGCCCTACATGCAAGGAACATCGTCAGG
CTACCAAACAAATACAACCTTTGGAATACACCAGATATCTTGCTAATTCACCTTAAAGGT
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTGATGCCACGGTTAATTTCCCATACAG
ATTTGGATCTGTGCGAGGTACGTTGTCTATAAAGATGATCCCAGAGGTTTAATCTATGACC
TGTATGCAGTAGATAAACCCTATGGTGGTTTGGGTGGTGGGCACTATACCGGTACGTAA
AGAATTTTGCCGACAATAAATGGTACTATTTTGTATGATTCTCGAGTAACTGAACTGCGC
CAGAAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTTCGCCGTACATAAAGATG
GCAATGGATTAGGCAGCTCTAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG
ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG
ACGAGGAGGAAGATGTTTTCTGATGATGATAGATGAATGTAATGAAGATGTGCAGGCCCTG
AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG
ATGACAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA
AAGTCTACAAGAATAATTCAGGCTTGGGTTTCATCGAGTACGCTCTGAAATATCTGAGGGAT
GCCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)

MGSSDVSSRECSLVYNEDPDFTDGTTPCDRLGVLDLMNVLDDKDEIKQESVPVSDREIEDT
ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG
DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFNF

LSEIYGMTSGSPVVTNLVINQTTGELETEYNKWFRLHYLTEKQDGRKRRHGQDDSIMY
LSMSALNLVRDLVEKSMNLFFFEKADHLDVNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE
ITPLQFLELPIKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHWPSNYFAYNKLEPA
SGTTGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL
VQKLFQNRMSIMQRNAAFPSPSMFKSTIGHFNSMFSGYMQQDSQEFLLFLDSLHEDLNRI
IKKEYTEKPSLSPGDDVNDWNVVKKLADDTWEMHLKRNCVITDLFVGMKSTLYCPECQ
NVSITFPDYNVDTLPLPVDTVWDKTIKIFPMNSPPLLELEVELSKSSTYMDLKNYVGMKMSG
LDPNTLFGCEIFSNQIYVNYESTESNAQFLTQLQELIKPADDVIFYELPVTNDNEVIVPVL
NTRIEKGYKNAMLFVPPFITLKEDELNNPGAIRMKLQNRVHLSGGYIPFPEPVGNRTD
FADAFPLLVEKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQQFASNRTGP
NFWTFISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGLMQVDDEGDTGSEAKNFS
KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS
LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER
TITLDDCLQLFSKPEILGLTDSWYCTCKEHRQATKQIQLWNTPDILLIHLKRFESQSRF
SDKIDATVNFPIITDLDLRYVVKDDPRGLLYDLVAVDNHYGGLGGGHYTAIVKNFADNK
WYYFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSSKLQEI IQKSRHGYDERIKKI
YDEQMKLYEFNKTDDEEDVSDDMIECNEDVQAPEYSNRSLEVGH IETQDCNDEDDND DGE
RTNSGRRLRLLLKKVYKNNSSGLSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167)

TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGCATAGATTGTGAATAAATCATT
TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG
GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCACACTCCTTGTATGACTGC
ATACGCATAAAGAGGTGCCTTGCTGTAGGCGTATATGATCCTAAGCAACAGAGAAACCAC
GGTTCTCTTCTCTTCTTATTTTCGTTATTGTCTTCCCTTTTTACTATGGGTAAAGTCGCC
TAAAGCGGGGCGCTCACAATATCGCCGAGCTACAGCCGTTTTTTTTTTTTTGTTTTTT
TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTTCATCGATATAAA
GAACACTGTTCACTTCGATGTATCCGGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA
GTGGTAGCTGGTACAGGATCATGAGATTTTCACACTTCTTGAAGTACAATGCTGCCAG
AATGGCAAAACCATTATATGGACTACAGCGAGCTGAAAAATCTTATTTACACGCTACAAA
CAGATGAACCTCAGGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAGAGCTCTAACA
TTACAGATAGGTTCAAAAACAAGTTTTCTTTTAAAAATGCGAAGGAAGATACGCTTCCG
GTATGAACAAAGATGCAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTTGCCACTG
CTCAGACGGTCGCTGCCAAACCTTCTCCTTTCAGAAGAATGAAGGAAAAGATATTTTACA
AAAGAAGGTCGCTTCCGCATCGTCCGCTCTCTCCACGGCCAACGAAAATCTGCAATTAG
ACACTTAGTATACGTTTGTGGTGATTTAACAGCTGAAAAACAGAAAGTAGATGATTTTT
ATAAGAGGACAGAAGCGAAGTTCTACGACAAAATTTGACGCGCTGGTGAAGGACCTGAAGA
AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAAACGAACCGATTGCCA
GCACAAATGACGAAGTTCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT
ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTCGCAGTATAACA
TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAAGTCGATCGTAAACCTATATATCGATCTTT
GCCAGTTGAAGTCGTTTCATCGAATTGAACCGCATTTGGGTTTGCAAAAATTACAAAGAAAT
CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACGATCGAATCGGAGCAGTTTTTCA
AAGACACATATGCATTCCAGGCAGAAACGATCGAATTGCTAAATTCCAAAATTTCCCGC
TAGTCACATTTTATGCGCGCATCACTGACCGGCTCATAATATCTCGCATAGCAAGCAAG
AGTTGAAATCCTACCTGCATGACCACATTGTTTGGGAAAGAAGTAACACTTGGAAGACA
TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAATATAATGCAA
ATAAGCTGGTAGGCAAGTTAGATTTGGAATACTACAGATGGCCACTACCCAGACCGATAA
ACTTAAAAATTCAGTAGTATAAACAACGTTGCACTACCGAAATTATTTTACCAAGAAAG
CATACAAGATTACTTTATTATTCTAGTCACTGGACTCTTGTAGGAATAAAGACCTTCA
ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTGAGTGTGTCGCCTTTTGTGGCGTA
GTGAGGCCATCCCATTAACATTACAGCATTCCCTTGTACCACTACTTGTAGTCCTTTTCA
AAGTCCTAAAAACCTCCGACGGGGCTATAATGAGTGCTGCAAGCGCTTCATCAGAAATTT
TGGCCGCCATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG
TACTTGCACAAATATAACATCGCCAAAGTTCTTGCCTCGTGGTTGTTGGCCTTCGCTGGTT
GTAAACCCAGAAACGTTCTTTTAAATGGCAATGTGTGTCGTGTTCTTCTATCAATGTGGA
TTTCCAATGTCGAGCACCTGTTCTAACATATTCGTTGTTATCTCCCTATTTGGATGCCA
TGGATCAGTAGCCCATTTGCGCAAGCATTTGGTGTAGGTGTAGCGTTGGCTGCAATA
TCGGTGGTATGTCTTACCAATCTCTTACCTCAAAACATCATTTCCATGTCTACTTGA
AACCTATGGTATTGGCTGGGGCCAATCTTTGCTGTTGCATTGCCATCTGGTATCCTGG

CCATGCTTTTGGTTTGGATTTTATTGTTCACTACTTTCAAGATGAATAAGACCAAATTGG
AAAAATTTAAGCCTATTAAGACGAAATTCACAGTTAAGCAGTATTATATCATTACTGTCA
CTGTGGCCACTATTTTGTGTGGTGTGTGGAAAGCCAGATTGAAGGTGCTTTTGGGTCAT
CAGGTCAAATTGCAATCATTCCCATCGTTTTGTTTTTGGTACCGGATTACTATCAACAC
AAGATTTAAATGCCTTTCCGTGGTCAATCGTTATTTTGGCAATGGGAGGTATTGCTTTGG
GGAAGGCCGTCTCATCCTCGGGTTTGCTATCAACCATTGCAAAAGCATTACAAAAGAAAA
TTGAGAATGATGGTGTTTTGGCATTCTATGTATTTTCGGTATCCTGATGTTGGTTGTGG
GTACTTTCGTCTCGCATACAGTATCCGCTATTATCATCATTCCCTTGGTGCAAGAAGTTG
GTGACAAGCTTGGCAACCCCAAAGCTGCTCCTATCCTTGTTTTCGGTGTGCAATTATTGT
CATCCTGTGGTATGGGACTAGCTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAG
TAGATAGAAAGGGCGATCGCTATTTAAGTGTGATGACTTTCTTAACGAGAGGTGTTCCAG
CTTCTATTTTGGCTTTCTATGTGTCACTACTCTAGGTTATGGTATCATGGCATCTGTTG
TCAAGGGTAACGCAACCTCTGCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAPPEWQNHMYDYSELKNLIYTLQTDDELQVGDNEEGFGAGKSSNITDRFKN
KFSFKNAKEDTSSGMNKDAGIVEETIELRELPTAQTVAAKPSPFRMKEKIFYKRRSSSA
SSVSSTANENLQLDITYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY
DIDDDTLFNEPIASTNDEVPPDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS
LLKKSIVNLYIDLCLQKSFIELNRIGFAKITKKSVDKVLHNLNTRTELIESEQFFKDTYAFQ
AETIELLNKESIQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ
ADELTPKETEYNANKLVGKLDLEYRWPLPRPINLKFTSINNVALPKLFYTKKAYKIYFI
ILVTGLLLGIKTFNDAAQHRCMALVECVAFWLWASEAIPHLHITAFVPLLVLFKVLKTS
GAIMSAASASSEILAAMWSSTIMILLAGFTLGEVLAQYNIKVLASWLLAFAGCKPRNVL
LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP
ISSPQNIISMSYLPYIGIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKEKFKPIK
TKFTVKQYIIITVTATILLWCVESQIEGAFSSGQIAIIPIVLFFGTGLLSTQDLNAFP
WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFVSHT
VSAIIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVTASIKVDRKGR
YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATTCTTTGAAAAGATTATTAAGTTCGTGCTTAAGTTCGCAATCT
GCATTTTCATTTAAAGACGGATCATATATTCTTGTGCTTTTTTGTTTTATCTCTTTACTTA
CTGTGCGCTTCCATTGCTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCCCTGGGCC
TCTGTTAACGTGAATAATCCTTGTATCCACCTGCCGACTCTGCTTGCTGCTCTTTGAAATC
GTACCAGAACTGAGTTGGCCTTATCTACATTTTCTACTCATTTTGAATGCACAGGTATCTG
ATTACTGATGTGGTGGCCTTGGCATATAACGGTGTGTCACTTTTATTTGCTCTTTTCATG
CATCCTGAAATTATTTACCCGCACTACGCAAAGAGAACGGAGAAAAAGGTATAATAGGGC
AAATGATCATTGACATCGTGATCGTAAGCCAAAAAATAACAATAGGCTCCCTAAATAA
GTAGAGTAAAAGCTCTTGAGATGAAGGAGAATGACATGAATAATGGCGTAGATAAATGGG
TAAATGAGGAAGATGGTCGAAATGATCATCATAACAACAATAAATACTTGATGAAGAAGG
CCATGATGAACAATGAGCAAATGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT
TGAGGAAAATATCAAGTGAAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTTCAT
CTCTCGTGAACGGCAATGCAAAACAGTGGCGGTGGTACGAGCATTAACGGAACAAGAGGAA
GTTCTAAGAGTAGTAATACACACTTTTCACTATGCCTCCACGGCGTATGGTGTAAAGATGT
TGAGTAAAGATATATCTAATACCAAAGTGGAACTGGATGTGGAAAATTTGATGATTGTTA
CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTTGG
TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG
CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA
AGGATTTTCATCAGGGAACATGATGTTTTCTTCGATTGGTAGTGACTTTGGGTGGCGACG
GTACTGTTCTTTTTGTAAGTTCCATTTTTTCAGAGACATGTACCACCCGTTATGTCGTTTT
CATTAGGGTCTCTAGGATTTTAAACAAATTTTAAGTTTGAACATTTTCAGGGAGGATTTAC
CTCGGATTATGAATCATAAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGCACAATTT
ATCGTAGACACCGCCCTGAAGTAGACCCAAACACGGGGAAGAAAATATGTGTGGTGGAAA
AACTAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGGTCCAAGTCCTTTTC
TATCCATGTTAGAATTGTATGGTGACGGTCATTAATGACCGTTGCGCAGGCGGACGGAC
TGATTGCTGTACTCCGACTGGGTCCACGGCCTATTCTTTGAGTGCAGGTGGGTCAATTTG
TATGCCCAACCGTCAATGCAATCGCTTTTAACACCCATTTGTCCACATGCATTGAGTTTCA
GACCCATCATCTTACCAGAAAGTATAAATTTAAAGTGAAAGTCTCGATGAAGTCAAGGG

CTCCAGCATGGGCGGCTTTTGATGGGAAAGATAGAATTGAATTGCAAAAAGGTGATTTTA
TAACCATATGCGCCAGCCCATATGCTTTTCCAACCGTGGAAGCCTCGCCCGATGAGTTTA
TTAACAGTATCAGTCGACAATAAAGTGAATGTGAGGGAACAACAAAAGTCCTTTACGC
ATATTTTGTCCAAAAGAACCAAGAAAAATATGCACATGAGGCGAACAAAGTCAGAAATC
AAGCAGAACCCTTTAGAGGTAATAAGAGATAAATACTCTCTGGAAGCAGACGCTACTAAGG
AAAACAACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAAACTGCGAAGCTTGCA
AATTAAAGCCTTCGAGCGTCCCAAAACCTTCTCAAGCAAGGTTTTTCAGTATAA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNGVDKWNEDGRNDHNNNNNLMKKAMMNEQIDRTQDIDNAKEMLRKISSE
SSSRSSLLNKDSSLVNGNANSGGGTSINGTRGSSKSSNTHFYASTAYGVRMLSKDISN
TKVELDVENLMIVTKLNDVSLYFLTRELVEWVLVHFPRVTVYVDSELKNSKKFAAGELCE
DSKCRSRIKYWTKDFIREHDVFFDLVVTLGGDGTVLFVSSIFQRHVPPVMSFSLGSLGF
LTNFKFEHFRDLPRIMNHKIKTNLRRLRECTIYRRHRPEVDPNTGKKICVVEKLSHHI
LNEVTIDRGPSPFLSMLLEYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMSRAPAWAAFDGDRIELQKGFITICASP
YAFPTVEASPDEFINSISRQLNWNVREQQKSFTHILSQKNQEKYAHEANKVRNQAEPLV
IRDKYSLEADATKENNNGSDDESDDSVNCEACKLKPSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2:
877-1255 (SEQ ID NO 171)

AGGTTGTGTTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCTGAGCAATAAGGT
AACAGCGAAATTTATGACATATTATTTCGAACCTTTTACAACTAGTAGATTTAGTGATT
TATTACCTATTGGCATTCAATTTGTGTCTATATGTGGATGAGGATAGCCGCTTTCTTCT
CATCGGAGGCCATATCATCTTTGACAATCCTTTTTAAATACTATTTCCATCCGTGCCTC
TAATAGATTTGTGTAGTTGTCTGGGTGCAATCTTTCCATTTTTGCTGAACTTTTTTTTT
TTTTTCATGTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT
GATCCGCCTCATACTAGCCATTACCCATCTATCCAGGCATTATGGGTATGCAACTCATA
ATCTCAAATAACAATAAGAGCAACCTTATATATCACTTTTTTCCCGTTCAGCAAGAGGT
AAAGCCACCAAAGGTTCAAATGCAAATGTATGTTACGGCGAATACAGAATACTATGTTTC
GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGGAAA
ATGATTGACAAGCTCACAATTTATTAACAAGTAGCAATTGAGAAAACTATTACTCGCG
GCAAGCTTCTGAGTTTACATTAAATCTGTAGAGCAAATTGAAAATGTTCGCATATGTGCTG
AAGGGTTTGTGTTCCATCTTATTTGCATAACATAGTTATATTTACTTGGTCGCATAA
AAAATATTTTTACTAACGTGAAGTTCTTTTCTTTATGATGTACGCACGCACGCTGTGTC
TTACTCCATAAATGAACCTTATTTCAATTTTGTACAGCTTCGTTAAGACTTTGACTGTAA
GACCATCACTTTGGAAGTTGAATCTTCTGACACCATTGACAATGTCAAGTCCAAGATCCA
AGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA
AGACGGTAGAAGCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT
GAGATTAAGAGGTGGTATCATTTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACGTG
TGACAAATCTGTTTGTCTGTAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG
AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQRLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGIIEPSLKALASKYNCDKSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAACAATACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTTCAGTC
AAGCCATGTCTTTACTTTCGTTTTAATGTTAGAAACAATCGCTTATTTGTTTTCTTTAAACA
AATATATTAGGTTCAAGGTCTTCGCAGGTGTAAGAAAACCCGTGGTCTCCATATTCTTAA
GTATGATAAATAAAAAAACTTAATAAATTATTAATTGCTTCAAACCTTTTTCTTTTTT
TAGTTTTTAATATTTCAAACGTATCTTCAATTGAACGCCCAAATAGGGAAAAATCCTGGC
AAATTTTTTATTGCTGTCAATCAAGGCTATGCTAGAAAATTCAAGAGCTTGGATGATTTA
AAAAGACACTCTCAATCGAGAAAGTTATTCTTTGTTATTCTGCTTTACCTGATCATATT
CCGGCGTATTGTTTCTAATCAAGTGATTTTCGATATCCAGTTACGAACCATTTACAACATT
CCTGAAAATATTGCGTATCAATGATATTTGCTCCTTCTTTCTCCCTCATTAATAATATTC
TCCTGGTAAGCTTTCTAATCAGCCACAGTTTTGCTGCCAAAACCTTTAACGTCTAGTTCCA
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATCTTTCATGGAGT

TTTTAAACGATTTTCGACACCGCTTTTCCACAGTATACCTCATACATGATGCAAAACCATT
TAACCTTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAG
CAGATTTACAATCTGATATTGCTCAGAGTTTCCGTTCACTCAATTCCAAACATTCATTA
CGGCCTTTCCATGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTC
CCCAACACTTCATAACAGGTGAGACAGAAGCTACCATGACTAACTCATCTTATGCCAGCC
AAAAAACTCCGTTTCCAATTCTGTTCTTTCTCGACAGCGAACGCAGGCCAGTCCATGA
TTTCCATGGCTAATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACTCTCTT
CAACATCCAGAACTAGTCAATCACAGAATGGTGCCCATGCCAAAAGCTTATATTTCCCCA
TGGCGTTGTTCCGAATCTTTGCAGTTGCCCTTTAA

YLR040C, 224 aa (SEQ ID NO 174)

MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDDTLARSAAADADMAFFMEFLNDFDT
AFPQYTSYMMQNHLTLQPVDYHHMVDLASTADLQSDIAQSFPTQFQTFITAFPWYT
SLLNKASATTIYLPQHFIETGETEATMTNSSYASQKNSVSNVFPSTANAGQSMISMANEE
NSTTALISASNSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:
950-1618 (SEQ ID NO 175)

GCACCTTTTCTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTCAACACTTTT
AATATTTCCCTTTTACATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT
TACCTATTTCTTAAAGGCCTTTGTCACTTCTTTATGGGAATGGCGCTACTTTAATTTTCC
GCCTACTTTGAAAAATTTACCAAGGCAGAAATGAGTGCGCTAGGCGGAAGTTCAGGGCA
CGGTCACCGAACCTTTGTGCTGTTTGAACGAGGGTCCCGCTGGAGGTTGACGGACGCGG
GAGGAGCTGGAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCTGGTAGG
GAACATCACCTTCTCTAGTTCTGTAAAAATAATATGATCAAGTTTGAATCCTCGTATTG
AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAGAAGAGATAA
GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTTGACTCCAGAGGATG
CCCAACTTTTGTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC
ATATCCCATACGATTATGTTCTATAGATGATAATAGGTCTCGAAAAGAATATGTCCCGCA
TTTAATCATATTTGGAGGTCAGAGGACCAAAGGTAATTTAGAGGAATTTGAACACGCC
GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAACTCAATAAG
AATATACATCCTCGACTGTGTCAAAGATTATGAACTCCGATGAAACAGTAAACGTCAAA
AAATTCCACGGGATATAATTCGGTACTTTATTTGATATGGAAGAAAACATTATATATGCA
CAAATGAACGCTCTTACTAACATAATTTATCTTTCTCTCTTTTTTTAGGTCCACCAAGA
ACCATACGTTTCAATGCTAGACCAGATGGTGTTCACGTTATCAATGTTGGTAAGACCTG
GGAAAAGTTGGTTTGGCTGCTAGAATTATGTGCTGCCATTCCAAACCCAGAAGATGTTGT
TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG
TGCTACTCCAATCGCCGGTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTT
TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA
GGAAGCTTCTTACGTTAACATTCCAGTCATTGCTTTGACTGATTTGGACTCCCCATCTGA
ATTTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTAATCTG
GTACTTGTGGCTAGAGAAGTTTGTAGACTAAGAGGTGCTTTGGTCGACAGAAGTCAACC
ATGGTCCATCATGCCAGATTTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC
TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGTTAAGGAAGAAGTCACTGA
AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)

MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAIPNPEDVVAISSRTYGQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDRPLDAQAIKEASYVNIPIVIALTDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE
VLRLRGALVDRTPWSIMPDLFYRNPEEVEQVAEEAAAAEEGEEVEEVEKEEVEGQAEAT
EWAEEENADNVEW

YLR088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)

CTTCCCATGTAGAATATCATTGTCAAACATACTACTACCGTGAGAATCCAATCTACTAAA
AAGACCCAGCTAAAGTCCTTTTGGTGTGTCAATGGAACACCACGTAATTGTGAAATAGCT
TCCATGCTTGTCTAACTTATTACCGTCAATAGAAGACTTGAGTCAGGTGGCTTTAATGAGT
ACTATCTTTTTTTTTTTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTTTTG
AGTATCCTGTAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCCAACAGCTTTATAGTGG

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG
CATCGTGAACCTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACAATACACGC
CGGCTACACTTAGAAAGAAATGACATTTGCTGTCTTATAAAAGGACTTGACAGACCAAAG
ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA
TGGGGCTTGTCCCGCGTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT
TTGGGTTTATTTCTATAGCTATTCTGCCCTATGGATGGACAGTACAGAAGACATACATTT
CTGAGAATGCATTGATGCCTTCAACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA
TTTTGAGGGGCTATCGATCTCAAATTAAGAAATGGTAAACATGACTTCTATGGAAGAA
ACAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG
ACAATATGGAGAAACATTGTACGGTGTAAATGCACGCTCCTAGGGGTGATGGAACAGAAG
CGATGGTGTGCTGCCGTTCCATGGTTTAAATTCAGATGATGAATTCATATTTGGCGGCGCAG
CTTTGGGTGTATCTTTAGCAAGATTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA
TTGTTGTCTTTCAGCGAAAATCCTCGTGCAGCATTAAGATCATGGGTTGAGGCATACCATA
CTTCTTAGATTGACTGGTGGTTCCATTGTAAGCTGCTGTTGTGTTGGATTATTCGAGTA
CGGAAGATTTCTTCGAGTATGTAGAAATCTCATACGACGGTCTGAATGGTGAGCTGCCCCA
ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT
TGCACGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAATAATAT
TATGCCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTAAAAAGCCCCATGGTAACGAGG
CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAAACAGTGGTCATG
ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG
AAAAATTTACCAATCGTTCTTCTTTATTTGTTATTAGCACACGTCAGTTTCGTATCCA
TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTTCGCCATAAGTTCAATTA
ATGCATTTATAACAATGCTTATGCAAATATATCCTTATTTTCCGAGTATAATTTGGTAG
CGTTGTTGGTTTGGTTCGTGTCTTGGTGATATCATTTGTTGTTTACAAGCGTTTCTTC
TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA
TACTTTCCAGAAAAATTCACATCTCAGAACCCTATCATACAGGTTGAAAAATGTTGCTT
TTTTATATTTTCAAGTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC
TGATCGGCACATTGGCATTTCCTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG
AACATGAGGTGACAACTCAATCCTCTAACCCAAATAAAAACTGAGCCGAAAGATGAGATTAG
AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAACAAAAAC
TAAAAAATTTAGTACTATTAATTTGACAAATCCATTTATTTCAATAACCTTATTCGGAC
TATTTTTTGTATGATGAATTTTATGATTTGATATAATAAACAACTGGTTTCAGCATGGT
TGGATTTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT
TGATATTAGCGTCATCGTTTGAATCTAAATCTGTCTAGTAAGGTGAAAGAAAGCAAA
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIIALLPVISMALCALFGFISIAILPMDGQYRRTYISENALMP
SQAYSYFRESEWNILRGYRSQIKEMVNMTSMERNNLMGSWLQEFGTKTAIYENEQYGETL
YGVMHAPRGDTEAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIIVFSEN
PRAALRSWVEAYHTSLDLTGGSIEAAVLDYSSTEDEFYVEISYDGLNGELPNLDLVNI
AISITEHEGMKVS LHGLPSDQLTNNFWSRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHGNSGHDITTFGRIPAMFRSINNLEKFHQSSFFYL LLA PRQFVSISYLLPS
AVALSIAFAISSLNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFLLI PSSGL
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFSLVSTSLLMINFAMALLIGTLAF
PMTFVKTI VESSSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLKNLVLL
ILTNPFI SITLFLGFFDDEFHGFDI INKLVS AWLDLKCWSWVFLCIGWLPWLLILASSF
ESKSVVRSKEKQS

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAAGATAGCTTGATCATCCTAAGCGGGTCGCATTTTACTATCCCCAGTTCCG
AAGAATAACAAGGCTCAATGCATATGCTGTTTATCGTGCTCACAAGGCGGTATGACGTTT
TTAGCAATGTAATTATATTA AAAAGATCTTCAGTCACTATGAGTGGTTGATTGCCCCATA
GAGAGCTATAAGCCGACGTGAAAGCTGCTGGTTCCAGCTTGGCTCATGTCGTCACCAAGTC
ACTAGTCACTTGGTCGCATTCAATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA
CTTGCCCAAGGGATTAGAATCACGTAAGACTCTTGATCCTTAGAAGATATTTCTGACAAAG
AACCACCTAAGCCATGCAAGTTTTTTTTTTTTCATTTGGTGGCGAAACAAAGGTGATGAAAG
TTTCTTCTTGTACAAACGCCAAGCCGATAGGTGAGACAATTTCTTGAAAGTAATGAGCTC
TGAGTAAGCATATCAGTCGAATGAAGTTCCAATATGCGTTGGCCAAGGAACAGCTAGGCA
GCAACTCGCGCAGTGGCGTCAAAAACTAATAAGTA AACACCACTGGCTTCCGGAATACT

ATTTCTCTGATCTCTCATTTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAA
CTACAATCATATCTTGTATGCGGCCCCGCAAACCAAGAGATTTATCCTTTGAGACATTGTG
AGACCCCTCCGTTTCGCAACCGTGCTCTCTGTTTTTCATCACTATATGCACGCTCTTTCCAAA
GCTCCTGCACTTTGCACGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA
CCTAA

YLR159W, 114 aa (SEQ ID NO 180)

MKFQYALAKEQLGSNSRSGVKKLISKHHLPEYYFSDLFSVQWDSRAIEKTTIISCM
RPNQEIYPLRHCETLRSQPCSLFSSLYARSFQSSCTLHVAEPSPGFHMYGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181)

ATCAAAAGAGTGTTCAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA
GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT
ATCGATAATAAATATTCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGCATCT
ACCTGGGGTTAATGAACGAGAAGTTCCTTGAGATATCTTTCCTGTTTACCTCCGTGCATCC
TGTAAGGAATTGGGTTTATCATTTATCATTTATTTTAGTACAACTTTTTTTTTTGGCCC
GGGCGCACTTTTTCAAGCGGTGGGAACATCAAAATGAAAACTAGATACTTTTAGACT
TATTAAATGGTTTAAATATTTTGAGATGTTTCGTTATATCAGAACTTCCTTACTTCTATC
TTTTATTCCAATACAAAGAAGTCACAAGATTACTTGGTAAGAAAGAAGCAGTTAATTTTT
AATTTTGCCGACAAGCCAAGATGCAAATTTTCGTCAAGACTTTAACCGGTAAGACTATTA
CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG
AAGGTATTCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGAAGATGGTA
GAACCTTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTGGTCTTGAGATTGA
GAGGTGGTGGTAAGAAGAGAAAGAAGAAGGTCTACACCACCCCAAAGAAGATCAAGCACA
AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCTTACTACAAGGTGATGCTGAAGGTAAGG
TTACCAAATTGAGAAGAGAATGTAGCAACCCAACTTGTGGTGCTGGTGTTCCTTGGCTA
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCAATTCGCTCTACAAGGTTAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQESTLHLVLRRLRGGGKKRKKKVYTPKKIKHKHKVKLAVLSYYKVDAEGKVTKLRRE
CSNPTCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)

AGCCACCAATTCCACCAGGCCCGGCATTCAAGTACTTGTAAGAACACCAACAGGCAAAGT
CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC
CAACCAATATGTGCGGGAATTGGTGGGCAAATGAGGTGATTCGGCCAATATCGAAATATT
GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCAATTCATCTTGATTTACCT
CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT
GAATAAAAACATTCTCAGGTTCCGAAATTCATGAATTTTGCACTGGTTGTAGAAAGCAT
AATAGTCTGATGGAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGTAGGTT
TATAAACGTAATTAACAATGAATTCAAATTTGCAGTGAGACTATTCACTACTGCAACTT
CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGAAGAATAGGTAAGTCAATGCTGA
CCCAAGGCACCTTTCTCTGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT
CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA
AAGAATTCCCGCATAAGTACGTCACAGGCTTATCGTCGGACGATAGTCCCATGGATTTAA
ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG
CTTCTCCATAATTACCAGTTTGTTCCTTTTTCACAGAATATTTAGGCTTAATATGTA
CGTATTGA

YLR232W, 115 aa (SEQ ID NO 184)

MGASSGRIGKSMLTQGTFFLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFPHKY
VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIITSLFLFSTEYLGICTY

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)

GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTTAGGTGCCCTGCA
ACACTAGTCATGGTAACTTCGCAGTTAGCCCCATTTCTGGCAAACGGGAACCCACTAAAC
ATGAAATCATAGTTCTTTACATACATGTAGCCGGAATCCCTTGAAGTTGATCTGCCTCCT
CCTAGGATCTGTGAAACTGCCTTCGCTATAGAATTTTTCTCTGCGACACATAGCACTTTC
ATTATTGTCTATAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAGGTGCTTTC

AAAAGCGATGCCCTCTTTATTGACAGTTACTAATTGCGCCAACTGCTTTTTTTTATCAAT
GTGATTTTCGCGTTTACGCCATTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG
CCTGTATGATCCGACCGTTTTTAGCAAACCTTATCAGGGGAAAAAGTATATTCCATTAAAT
GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT
TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCGATG
AAAATGCATATATCACGTTTACAGATGCTTCCCTGGATGGAATACATCGCAAATCTACTAGGT
TTCTCGAAGAGCTACTTTTGAACAAGAAAATATGTACCATAATAACAATTACGAACGCA
TAAATGATTCCGTGATACCATTGGTTCTGAACTTTTTATGGCTTCAAATTCAGAACCTA
CACTCCAATGGTTTGGAGCACTGGTTCCATGATATCATGCGACTAAGTAACAGAAGAAAGT
TCAGAGTTTTTAGAATTTTTCAAAAAAAATGATTCAATTTTTCAAAATTACACACAGGT
ATTACTATGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCGGTTATTTCAA
ATGCTCTCTTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA
AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT
GCGTGATTAATCTAGGTTCCACACATTTTTATAAAACACTACTAAACAAGCCGTCTAACA
AACCAAGAGTGTGGAAGGTTTTGAGAAGTCTATTAGGTACTTGAATATTGCCCTCACTCT
ATCTCCCAGCCGTTGGAGATACTTATTTTCAACGAGCGAAAATTTACTTGATCACTGGGA
AATTCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTGGTAAGGATTCCGTCTAAAT
GTGCGTTAAACAATTTGAAAGATTTCATTTTGACTCCTGATTTTCCGGAAGAAGACGTC
TGATGAAAAAATTGGCAATTCTTGTGTCAAAGATCTCAAAGGTGAGAAATCATTTCTTG
AAGGTCAAATTTGTTTGAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCAT
GGAACGCATCACGTGCTTCTAATTGTTGGTTATTGAAAGAGCATTACAAATGGCTGCAT
TAAAGTATCATTACAGGTAATATTAATGTTATACCTTGAAAACCTGGCTGCCCAATGGGAA
GTTTCGATCTTATGTTTACAACCTCGAAAAAGTAAGGAACAAAAGAACAACTCAAATATG
CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTAGACTTGAGCTTTGATTTTATTGCTAATA
TCATAGACGTCGTCATCAAACCCCTCCTGGCAAAAAACATGGAAGACTTTCGATATCTAG
CCATTATTCGTTTGCTTATGTGCTGGATTAAAGTCATATAGATCTATTTTGCAGTACACTC
ACAGACACAGGAAGTTTGCACCTTCATTCCGCTTGTGCTGAACGACTTGATAAATAGTC
CACTGAATTTGTTTCAAGAAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTTAGAG
AAGATATTATTTTCAAGGAATTTTCTTGCAATTAACCTTGCCTAACAGATTTTAAAGAGC
ATTATGTGTATGATTCTCCCGACATGATTAAATAATATAATTGGATGCCCTACATTGACTA
AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTGGCA
TGAAATTTTTAGAGAAAAATGACACCGCGTCATATGGAATGCCAGCAAATATAAGTTTG
ATTTAATAAGCCCAATATTAATAAATAAACGCCAAATAGCATATCGGAAATTTCTCTCCA
AAATAAATGTAAAAACACAACAGGAAAGAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA
GAGATGAACAACAGCGCAAAAGAGCCGGGAAAATAGCTGTGACAGAACTGGAAAAACAAT
TTGCAAAATGTCGCGAGAACAAAAAATTTGTCTCCGCTCCAGAAAAAGATGGCGTTTCTT
CTGAGTTGGTAAACATGCTGCTTCACGAGGGAGAAAACTATCACTGGCCCATATCCT
CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG
TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)

MDNEEVNEECMRLFFKNARAHLDKHLTSRLTCDENAYITFRCLDGIHRKSTRFLEELL
KQENMYHNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKMKIQFFKITHRYYYDIIIEHLCAKYDMNSVISNALFAKLNLMOYTDGLSTHEKIILNTS
NPLTFSIVISLQRCVINLGSTHFYKTLNKPSPKPSVEGFESIRYLNIAASLYLPAVGD
TYFQRAKIYILITGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDFPERRRLMKKLAI
LVSKDLKGESFFEGQIVLQFLSIVEHTLVPQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSFDFLMFTTRKSKEQKNLKYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILQYTHRRKFCSTFALLLNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALDFNDYVYDSPDMINNIIGCPTLTKVLSPE
ECVLRIRSIIFSGMKFLEKNDTGVIWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSRKVEAKRDEQQRKRAKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASRGRKTIITGPLSSDFLSYPDEAIDADEDITVQVPDTP

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCACGGAATCATTTATGCGTTTCGTAATTGTTATTATGGTACATATTTTCTTGT
TTCAAAAGTAGCTCTTCGAGAAACCTAGTAGATTGCGATGTATTCCATCCAGGAAGCAT
TCGAACGTGATATATGCATTTTTCATCGCATGTCAACCTTGATGTTAGATGTTTATCCAGA
TGCGCACGAGCGTTCTTGAAAAATAATCTCATACATTCTTCGTTAACTTCTTATCC
ATTATCTATGGTGGCATGTGTCAATTAATGGAATATACTTTTCCCTGATAAGTTTGCT

MKVLCVAEKNLSIAKAVSQILGGGRSTSRDSGYMYVKNYDFMFSGFPFARNGANCEVMTMTS
 VAGHLTGIDFSHDSHGWGKCAIQELFDAPLNEIMNNNQKKIASNIKREARNADYLMIWTD
 CDREGEYIGWEIWQEAQRNRLIQNDQVYRAVFSHLERQHILNAARNPSRLDMKSVHVG
 TRIEIDLRAVTFTRLLETETLRNKLNRQATMTKDGAKHRGGNKNDSSQVVSYGTCQFPPTLG
 FVVDRFERIRNFVPEEFWYIQLVVENKDNNGTTTFQWDRGHLFDRLSVLTFYETCIE TAG
 NVAQVVDLKSPTTKYRPLPLTTVELQKNCARYLRLNAKQSLDAAEKLYQKGFISYPRTE
 TDTFFPHAMDLSLVEKQAQLDQLAAGGRTAWASYAASLLQPENTSNNNKFKFPRSGSHDD
 KAHPIIHPIVSLGPEANVSPVERRVYEYVARHFLACCSADAKGQSMTLVLDWAVERFSAS
 GLVVLERNFLDVPYHARWETTKQLPRLEMMNALVDIAKAEMKAGTTAPPKPMTESELILLM
 DTNGIGTDTATIAEHWIDKIQVRNVRSEKVGKLTLYQPTTLGVSLVHGFEAIGLEDSFAKP
 FORREMEODLKKICEGHASKTDVVKDIVEKYRKYWHKTNACKNTLLOVYDRVKASM

CTTCGTTACACTTAATATTAAATAACAGCTCTTTTCCTAATAATAACATATACACTAGAT
ATATAATACCAAATAAATTAAAAAAAAGAAAAACAAAAATAACGTAGCTTTGTTACAG
TCGTAAAAAAAAGAACAATAAACCAATCTTATTGCCAGCGTCTAACTAGTCCTATTATAT
TCCAATATATTAAAGGGTAAGGACTACTATTATTCGCCCTGAATTGAAATCTTTTAGAAA
GCACCTGTTTCTCTCTCTGGTGTTCTTTTTTCTCATCTATTATCTAATTTCTTCAACCTT
CGTTATTGTTGTTATTCCGTAATCGTGGTGCTCAACTTTTGAATTTCACTTGTTTACC
ATAACGGAAGATAATTAATAAATTTGTTCTTGAAAGTCACAAGCACTACGTGAACACAAAA
TTAAGGCAAGAGTGACAAAGTAACCTCAACAGGAGCCTGTCGTTGGTTATATTGGAAGC

TATAGATATAATCGAATCCAATGACTGGTCCTGGACCTGAAATAAATAAGGAGGAGCACC
CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA
TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAAATAGCCG
ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAAATATACTT
ACATTC TAGTCCTCACATCACTAAATGGAACCTTTTGAGAGCAAACATGTGGTGATACCAT
TTAAACCAAGATGGTTTGAAATTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT
CATCGCTCAGGGGCGGTAAAAGAGTGGATTACACACACTTTTTCCCAAGTAAGTCCGATA
ATGGTAATTTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCGACCCGC
TCACGGGTAAGGTATATATACGAGACTTAAAATCCAGTAATGGTACGTTTATTAACGGTC
AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGGAACAG
ATATAGATACGAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAACTATTTGTAC
AACCTTTATTAGAATCACCGATTTTGAATAAGATAGTGATGATTGCCATACAATTA
CAGAAAAAGAGGAGGCTGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG
AATTGGAAGAAGTTATCTTGGGCTCTGATACAGAAATACTGAGTGAATTTTATTATAA
ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATGGAAATTC
CATTTTCCAAATGCGATAATTTTAAATTACAGTCGATGGAGAATTTCTTAATTAATTATA
CGACACATCTAGAATACACGAACAACTTTTAGTGGAATAAATGATCAGCAACTGGTAA
AGCTGCAAAATGGATTAAGAAGGAACTGTCTGGGGAATAACGAAAAGATTATCGAACAAA
ACAGAAATCAAGTAAAACAGTTGGAAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG
TGAAGAAAAGAAGAAATAATGAAAAGCAAAAAGCATGGAAGGGGAAATAGAAGACTTGA
AAACTAGGTTAGAAGTGAACGATATAAGAATTCACAAATGATGAAGAAGAACAAACAGA
AAGAACAAGAACCTCAACTGCATCTAAAAAAAGACTACCGAACATGACACTAGAGGCG
TCCCGGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC
ATTTACACTATTAACATTTGGAATTTCCATCGGGATTATAGCTATTGTCTTCAAGA
TCCTTTCCCCCAACTAG

YLR238W, 478 aa (SEQ ID NO 190)

MTGPGPEINKEEHPSSPGKKQITYNSIPKNaNLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKYTYILVLTSLNGTFESKHVVI PFKPDGLKLGRPVANSNSSSSSSSLRGGK
RVDSTHFSQVRSDNGNFDNRVLSRNHALLSCDPLTGKVYIRDLKSSNGTF INGQRIGSND
VEIKVGDVIDLGTIDIDTKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLEEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTTTHLEYTNKLLVEKNQQLVKLQNLRRKLSGKYEKI IEQNRNQVKQ
LERDHMF FKKSFVKKRRNNEKQKSMEREIEDLKTREVERYKNSQMMKKNKQKEQELST
ASKKKTTTEHDTRGVPGMNPKGTDKFSIKNTLCNHFTLLTFGTISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191)

CGAACATACCTGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGAT
TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCATTTTTCAGAATCTAATCAATGATA
GTGTAATGCTTTGCTGCCTATCGTGATTGATCATTACATAATCTGGCACAATACTGGC
GGACCTGATTGGTTGATAATTGGTGCTTCAAAATTTAAATTTTCGTCACTCTAATTATACT
TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT
AATTGCACTTTTTTTTATTTAAAAATAAAAAATCACAGTTAATTTTTCATGATCTTGCAAA
GACACGCCCTCCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAAACTCAACACTT
TAACATAATGGCGGGCACGAAGGCTAAACAACAAGATTAGCATTGAATGCCTTTTGTGG
GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT
ATCTTGATACAGTTCCAGATGAGCATCATGATTTTCAGAAAACCCACCGCCAAGGTTGTAA
CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTGTCTTTGCTTTTCGTTCTCAATTC
TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC
GCTTACCGTCTCGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTGTATTAAGATAC
GGGACGAACAGATTCTGGAATATGACAGGTTTAGATGCGTATGTGTTTTTGTGTTTTTCA
AAATGTGCATCAAAATTAATTTCTATTTTTTGTCTTCTCTGTGTGCGTTATATCTCCAG
TAAGATATCATTTTACTGGAAAAATGATGACGGCAACGATGATGATGACAGTGAAAGTT
CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG
CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTCTTCACATATTTCTTCACCT
TCATAGCAATTAATGGCAGTTGCGGAAACAAAGCACGTCGTAAGTACTAGGCAAGCTT
ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCCGATAG
AGCTTCGTGATTCGGAAGCCTTAAAGACCAGAATTGAACAATTAAAAATCGGACCGTTT
CATCAATCACTATTTGTGAGAGTGGGGTCTTTGAACAAGCTATTTTCATTGTGCGGAAGA
AAATACTCAAAAACCTGGAATTAATAATTCAGAATGTCCAAGGGAGCTCCGTACTCGAC

AACCATATTCGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG
GAGAAAAATGTTCCATCAAGCAATAATAATGACGAGGATACCTATACTATATTTCTCAAATTT
CTCTTGGAGAGAGACCAAAAATGAAAAATTGGATATCGTGGTATCTTTGGGAAGGAAGTAG
ATGCCATAGAGTACCTGGAGCAGCAATTAAATTTATTGATGCTGAAATTATTGAAGCGA
GGAAACAACACTACTCCGCAACACCTACGGCATTTCGTTACGATGGATTCTGTTGCTAATG
CGCAAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG
CTCCTGCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTAA
CAAAAGTTTATTCTACTACCGTATTTATAGGCCTTTCAAGTTTGTTTTATGTCATTCCTG
TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTCGAAATTCTGGCCAAGCGTAG
GGCAGCTACTAAAAGATCACCGTGGGCCGCTAACATTGTAACGGGGCTATTACCAACCT
ATCTCTTCACATTGCTTAACCTTTGGAATCCCTATTTTACGAGTATTTGACTTCTTATC
AAGGATTGGTATCATACAGCGAAGAGGAAATCTCACTTGTTCAAAAAATTTCTTTTATA
TTTTTGTCAACCTTTTCTTAGTTTTCACATTCGGCAGGTACAGCATCTAATTACTGGGCGT
ACCTCAGCGATACCACCAAAATTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT
TATTCTATGTCGATTTGATTATATTGCAAGGTATTGGTATGTTCCCGTTTAAAGTTGTTAT
TAGTTGGTAGTTTGATCGGCTTTCTCTAGTGAAAATCAAGGCTAAGACACCTAGGCAAC
GGAATGAACTTTACAATCCACCGATATTTAATTTGGACTACAATTACCACAGCCAATTC
TGATTTTGATTATAACGTTGATCTACAGTGTAATGAGCAGCAAAATTTTGACTTCAGGGC
TGGCGTACTTTATTATTGGGTTTTACGCTATAAAATATCAATTGATTTTTGCCACAGATC
ATTTGCCCTTCTACAGGAAAAGTATGGCCATTAAATTTTAGAAGAATCATCGTTGGAT
TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTCGAAGGAGGATGGGTTT
TGTCATCTTGCCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCTATATGATTTTCGAGA
AGAACTATTTGCCGTTGTCAAAATATATCGCATTGAGTTCAATTTCGCGAGTACGAAAGAG
ACAATTCTACGGTGAATTCTGCCAATGAGGAAGAGTCGTATGCATACCCCTACGCTGTGA
GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAASYLDTVPDEHDFRKPATKVVTTQLTIATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSSLFGWLTVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDDDGDDDDSESLIHLVKRIVEGSGDGDNHSAPERTNV
YLWMYVLFYFFTFIAIKMAVAETKHVVSTRQAYLGKQNTITDRITIRLSGPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPLNKLHFHCRKKILKNLELKYSECPRELRTROPYSENY
HLLGNEQSGAVTHGENVPSSNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLKFIDAEIIEARKQHYSATPTAFVTMDSVANAQMAQAVLDPRVHYFITRLAPAPHDI
KWDHVCLSRKDLTKVYSTTVFIGLSSFLVPIVSYLATLLNLKTLKFWPSVQGLLKDH
QWAANIVTGLLPTYLFTLLNFGIPYFYEYLTSYQGLVSYSEEEISLVSKNFFYIFVNLFL
VFTLAGTASNYWAYLSDTTKIAYQLATSVEKFSLFYVDLIILQGIGMFPFKLLLVGSLIG
FPLVKIKAKTQRNELYNPPIFNFLQLPQPILILIIITLIYSVMSTKILTSGLAYFIIG
FYVYKYQLIFATDHLPHSTGKWVPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSCLFP
LPVVTLCFLYDFEKNYLPLSKYIALSSIREYERDNTVNSANEEESYAYPYAVSELEGPM
LD

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)

TTCAAGTGCACCTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAACTGTGGCCAT
TATTTTTGTGGATCGTGTTTTGCCAAAGATATGAAAAGGGCACCAAATGCTTTATATGC
CACAAGGAGACCCACGGCAGTGCAAAAGTAGCATCTGACTTACAGAAGATGCTAAATAAA
AGGAAAAGTTGATGGAGAATGCCATATCACCCCAAAATACACGCACCCGATGCTAATG
TACAGGAATTATAGAGCACATGACCCATAGATTTATCGAGCATTGTTGCAATTTGAAAG
ACTCTTTTACATAATAAAGTATGTAACTATATAGATAGAAGATGTCCCGTGTCTTTTGT
TCTACTAAATGATGATCTGCTCATTTAAAGTCGCCGCGACTACTTTGACAAAAA
ACTTAGAAAATACGACAAATAGAGATTATTGAATGAAGTACATTGAAAAAGAAAGAAGA
AAGGCACATAGCAGCACACAATGTCGACCAAAACCAGCTTATTCCACAAGCTTATATTT
CTAACTTTTACATAACAGATTGACAAACGAAGATGATGGTATCCCATCTTTACAATGGCTC
AACAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC
TCTTTGATGAATTCATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG
ATACTGAGTGTCTCATGAAAATACTCCGGCACTTACAAATGGTGTACCATTGGACGGTT
CCGAATACAATGTCCTAGAGAACATGAATGGAGCTGATAGTATTATCTCTAAACAACAAAT
ACGATGCGGGTTCAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG
CCAGCAATGGTCCGAGCAACAAAGCGCAGGCACAGGATATTGGAACGCCGTCTACCGG
ATCTGCAAGACCAACACCACAACCCCTTCAACATATTGAGATACCTAAATAAGAGATA

CTTTCATTAAACGGAAAAGTGGTGTCTCCATATAGACTCAACACTGATCAAGAAACGAAGG
CAAACGCCAATTCTGGAGAGGCAATCATGATACCAATTACTTTGGATATAGAACATATGG
GTCATACCATAAAAGACCAGTTTCTCTGGAACCTACAATGACGACTCCATATCTCCGGAGG
AATTTGCCCTCTATATACTGTAAAGATCTTGATATGACTTCCGCTACCTTACAAACTCAA
TTGCGAATATAATAAAAGAGCAGTTGAAAGACCTCGAAAATATTGCAGCCACTGAGATAA
TGTCTGACCTCCACGTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTTTGAAG
ATAACTTCCAGTGGAACTTGAACGACAAATCACTTACTCCAGAAAGATTTGCTACATCCA
TTGTACAGGACCTTGGCTTAACAAGAGAGTTCATCCCCTTAATATCTCAATCGCTTCATG
AACTATCTTGAAGATAAAGAAGGACTGGGTAGATGGCCACTTGATTGAGGACCATGTCC
CAAACGATGCCCGATTTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACTGGGCT
CCAATTGGTGGCCAAAGGTGGAAATATTAACAAAAGAAGAAATACAAAAGAGAGAAATTG
AAAAAGAAAGAACTTAAGAAGATTGAAAAGAGAACTGATAGATTATCTAGAAGGGGCA
GGAGAAGATTAGATGACTTAGAAACCACAAATGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)

MSHQNLIPQAYISNFHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNYAEYDNDLDFDEFNM
NGSNFNADTHYKDNVSHENTPALTNVMTDGMSEYNVLENMNGADSIISNNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHNPFNILRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNYNDDSIISPEEFASIYC
KDLDMTSATLQTOIANIIKEQLKDLENIAATEIMSDLHVIINLTCNLQDRFFEDNFQWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKKDWVDGHLIQDHPVNDAAF
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRRLKRETDRLSRRGRRRLDDL
ETTMRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)

GTCATATCAAGATCTTTACAGTATATAGAGGCAAATTCCTCCGGAGATATGGAGTCGTCA
TTGTAGTTCAGAGAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATGCTCTCCAGAATTGGCGTTTGCCTTCGTTTCTTGATCAGTGTG
AGTCTATATGGAGACACCCTTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC
AATATGTTGAAGGGTGTGGTGTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCAATA
TCCTGTGCTGCGCTTTGTTGCTCGGACCATGCTGGCGTTGTTATTGCTATTCAAACCG
GATAAAGATTCACAAACCATGTTTGAACCCGCATCGTATTTGTTGTTAGAGATAATACTA
TCAGCTCCATTCATGTTCTCTAGGACATTGTATTCCGAACCGTCCATGGTAACACCATT
GTAAGTGCCGAGTATTTTCATGAGACACTGCATTATCTTTATAGTGTGTATCAGCATTG
TTGAAATTAGAACCCTTCATATTGAATTCATCAAAGAGATCGTTGTCATATTCGCATAG
TTGACCCTTTAGCCCTTTTATGCTGCTTGTGTTGTTGAGCCATTGTAAAGATGGGGATA
CCATCATCTTCGTTTGTCAATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC
TGGTTTTGGTGCACATTGTGTGCTGCTATGTGCCTTTCTTCTTTTCTTTTCAATGTAC
TTCATTCAATAATCTCTATTTGTGCTATTTTCTAA

YLR322W, 104 aa (SEQ ID NO 196)

MRHCIIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDITIFVCQ
SVMKVRNISLWNKLVLRHCVLLCAFLLSFFNVLSHSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)

CCACATGTCACAACTACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAAACATCATA
GCCTTGCCAAAATAACTCGCTTCCCAGAAAAGACGCCAAATTAAGTCCGCTGTTATGTG
ACAAAACAGGGCATCTCACATATTCGCGTACTGGTGTCTTTTAGCTCATTCGGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAAACCCACACA
ATTAATAATGCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAATAGACGGA
GCATCATACGTTTCGAGTGGAAAATTATGGAGAGTTTTCGAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTACGCTTTTGCACAATATGAATCTTCAATCTAAAGAATTAAATTT
TCTAATTTCAATGTAGAAATATTTCAACTGTTAGTTTTTTATTTTCAAGTTGAATATAGTA
CGACAAAATATCAAGGAAAAATGGCTAGAGAAAATCACCGACATCAACAATTTTGGGAAT
TGACCAGAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAAACAAAAAATTGAACAAGG
CCGGTAAGCCATTCAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTTGTACACTT
TGGTTATCAACGATGCTGGTAAGGCTAAGAAATTGATCCAATCTTTGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)

MAREITDIKQFLELTRRADVKATATVKINKKLNKAGKPFRTKFKVRGSSSLYTLVINDAG
KAKKLIQSLPPTLKVNRL

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:
967-1331 (SEQ ID NO 199)

TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG
ATTATTAGTTATTTGTTTGTTCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA
TCGATTACTTATGCTATTCTATTGTATTTGAGCCGGCGGCTAGTAAACAAGACAGCATAC
CTTCCAACATCCGTACATATTGATTATTTGTATCTATGATTTTCATGTAATGTATGGGTT
AACTAACTCTTCTCTTCTTTTTTTTTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTT
GTGAAAGATATGGAATATTCCGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG
GATGGAATCTTGCCCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCGAAGTACAAGAT
ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCGATTCTATATTATTGACGTA
ACCAACAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT
CACTGAAACCCCTGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTGCCCTGAGGGCAG
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA
CTTGTAACCTATTTAGGTGATGTCTCATAACTGCAACCACTGGAAAATGACGCAAAATATC
AAAAATAATAGGGAGATAAAGTCTCACGACATGAAAAATCATAGAATTATTGTTCAATTT
ATCTAGCCGTATCTTACCTTATGGAAAAAGTGTGAATATGTTTTTCTAAATCGAGCTTCC
CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTCTCCAAGG
TCCTGCTTACTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTTCATTA
TTTTAGACGTTTCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTACCGCCCCATCCT
CCCAACGTCGTGTTTTGCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA
TCAAGGCCCTTGCCAATCAGAAGAGATGATGAAGTTTTGTTGTTTCGTGGTTCCAAGAAGG
GTCAAGAAGGTAAGATTTTCATCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG
TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCCAATTAACCTTGACCCCATCCAAGCTTG
TCATTACTAAATTACATTTGGACAAGGACAGAAAAGCTTTGATCCAAAGAAAGGGCGGTA
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)

MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVGASVPINLHPSKLVITKLHLDKDRKALIQ
RKGGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:
1117-1376 (SEQ ID NO 201)

ACTTTTTGTCTGCTGCTGGTCTGTTTGTCTTTTCGTTTTTAAAATTGCGCTAGACAAGTAAAC
AGGGATTGCTTAAGAATCAAAGTAGCTTAACTCTAAAGTATTATTTTCTCAGTTGTGGG
CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCCGTTGAACT
TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTTACGCAATTACAACCGCATT
ATTTACCTTTTTCATCTTCAGTTTACGGTTCAGTTTATTCTGTTACGAAAGAACTATGGT
GATTCAAAGGCGAAGTGCGTAGGATTGTAACCTCCTATATCTTTAGGATACTTACAATTTT
GTACTGTTTTCAAGACCACGTGAACCGGATAATAAACCGGAGGACACATTTTAACCCACTA
TTTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAAA
ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA
TCATCAAGTTTTTACAAGTTATGCAAAAAGCATGGTATGTTCCAACCTATTTTTCAATATTT
TCACATGTGTTTTCAATTTCTGCTTATTTTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA
ATGTTGCGCAACTCTAACGAAGAAATAATATTGCCATTGTTTTTACTCCGGGCTGATA
ACTAGATGGTGTGATCGGGCAGTATACTAAATTTATACTGGACAAAGACTCGTAAAAGATG
TTCTTTGTGCTTAGTCCCATACTGTTTTTTAAGTGTCCGGGATATTTAATCCCATGTGGA
AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT
TACTTTTCCCTCAAATCTCACTCTTAAATTTTCAATGGCAAAATTTCTCCGCACAACCTT
AGACAACATTTTCTTGTTTTTTATGAAGTAAGCAAAAATTTTCAATCAACAACGCTCCAT
GAGATTCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTCGAATACA
TTGACGACCACAGATCTGGTAAGATTGTCGTCCTCAACTGAACGGTAGATTGAACAAATGTG
GTGTTATTTTCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCCCAACT
TATTGCCAGCCAGACAATTCGGTTACGTTATTTTGACTACTTCTGCGGGTATTATGGACC
ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAAATCTTGGGTTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIKFLQVMQKHGYIGEFEYIDDHRSRK
IVVQLNGRLNKCGLVSPRFNVKIGDIEKWTANLLPARQFGYVILTTTSAGIMDHEEARRKH
VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCGCATTTTGCTGAGAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC
CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAAATAAAATATCATGTATC
TCACCCCTCTTCTTGGTATTAGTAAAGAGACGCCTGATCTTGTAAACAGTGGTGAAGATTGT
ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAGGCAAGGCAGAGGCGATGTACATAAA
ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAA
TACTATAAACGTTTGT'TTTGTTCCTTACGCACAATATCCTTGCCCTAGAAATCGTT'TTTGA
AATTTAAATTTTATTACCATTATTTTGATTTCGCCTTCAGAAAAATATGGAAGAGTGCAT
ATTTAAAAAGGACTATTTTCAGCATATAGTAAAAGTCAGGTTATTTGTTTATTTGCGATAT
CAGAGTAACTTAAACTAATATGCAGGGCACTTTTAAAAGGTTTACCATCCCACGCTTA
CGCGGATGTCTTCTTGGATAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG
AATACCAGATCAAACAACCTGGTCAAGC CAATAGGCTTAACACAAGCACCAAGGAAAAGCA
CCAAATACTCCCGAGGGAACCTTTTGAGGGATATGTTTGATTTCGAAAAGACAAACCACA
GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAATCTGGACTTTATGACGTGCAAGTCTTCC
AAAAGACAAAGGGGAAATTTGTTTATAGCTCCAGTTTCATATTGGAAAGAAGATAAAGCTT
TGTTTTTTTCTCATTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG
ATATGTTAAGGGTAAAACCAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT
TGAGTAGTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAACTGACTACTTGACTG
AAGCTGATGCGCGTTTAAAGTTTAAATGACAGTAACGTCCAAATCATCGAGGTCAATCTTG
TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTC
CATCCTGGCGCCAGCCATTTTATTTTCAATGTTCTTAGAGGCCAATGGCCATTTTCCGTC
GGGAAGAGCTCTTTTGAATAATGTCTTTTCTGGATACGTCTTTCTTGTGGACCAGCAGT
TAAAAATTAGGTGGGAGCTTGCAGGGAGGCTACTCCATCTGAAAAGGAAGCATTGTGGA
AGTTTGCCAAACGTCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MOGTFKRFYHPTLTRMSFLDKFLKPMMATASPKYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVFQKTGKGLFIAPVSYWKEDKALFFPHLI
GTAMDGKQQNIEDMLRGKTSIVRLFSTASGDKLSSSYFQGI VDDNKKTDYLTADARLS
LNDNSNVQIIIEVNLVENAVKSALVKTLARWANRVPSWRQPFYFEC SRGQWPFSVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)

TTCTATTGGTGTAGTTATACCAGAACCATCCTTCCCAAGGCCCTTTCCCGCAACATATCC
CATACTCGAAAGTAACCTTCGCACCAATACCATATGTCTTCGTTAATTTTGAGATCGTTGG
GGCATTTGCCGCTACTAGTTTCAAGGCATCATTAGTGTATGTCATGTCACATTTTCATGCT
TGAATTATTATCTTCTCATCGCTATAATTATAGGAATCGATTCTTCTTTTTTTGAAAAA
GAAC'TTTTTATCTGTGTTGGAGTCCGAATCCTCCATGTTTGGCGTACTGAAGGCTTAAG
TTCTTCGACCTCTCTCGGTGTACTATTTTGAAATTTTGGATTTTGTATTGTTTGTGAC
ATAATGTAAATACTAGATGCGCGCTCTAAGGCCTCAGTATTAATAATGCAAGATATCCC
TAAC'TTGATAATTATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCGAGGATAT
TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA
GGAAAACGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA
TTAAGAAAAAATTTGTCATCTTGGCAGTTGAGTATTTCAAACTCAATTTTCTAATAGTTG
GCTTGAGACAGCAAGGAAAGTTTCTTTACACTATTTTAAAGGAAGGCATTGGGACAAAGC
TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT
GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA
TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAACG
TTAAC'TTATTGAATGACAAACTGAAAGAAGTGCCAGTAATTGAGCGTCAAATTGAAAACA
TTAAGCTTCAATACGAAAAATATGGTCAGAAAAGTTAACAAAAGAACTGATTGATACCAAGT
TGACGGACGTAAC'TCAAAAATTCCAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA
ATGTTGTCAGAGCAGTTTAGCAGGGAAC'TAACGGACCTTGAAAAAGATTAGCAGAGATAA
TGAA'TTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA
ACGATGAACGTGAGGAGCTGTTTAAAGTGGTACAAGGCGACGACAAAAGAACTATACAACA
TTTTCAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATTTCTTAAC'TTGGGTC

AATTTTTGCAGGCAAAAATAAAGGAAAAGACAGAACTACACAGCGAAGTTTCTGAAATAA
TAAACGATTTCAATAGAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAATTCCTGTACACAAGATATTCAAACAACTAAGGAACTTTGTGAAT
TTTATGATAATTTTGAAGAAAGCTACGGTAACTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAAATGAAAACATATTTGAAAGATTGTGAAAAGCAGTTGCAGAATTTAG
ATGCTCAGGACCAGGAAGAACGTCAGAAATTTTATAGCGGAAAATGGAACCTATCTTCCTG
AGACAATCTGGCCCGGTAAAATTGACGATTTTCTTCCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)

MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQOGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKEYQYEITSKVQRLDGIYNELSISEKDDT
DPSKLGDIYISRDNVNLLNDKLKEVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVTK
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTLILLQDKKIDNDEREEL
FKVVQGGDKELYNIFKTLHEVIDDVDTILNLGQFLQAKIKEKTELHSEVSEI INDFNRN
LEYLLIFKDISNLI DSFKNSCTQDIQTTELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCEKQLQNLDAQDQEERQNFIAENGTYLPETIWP GKIDDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:
949-1342 (SEQ ID NO 207)

ATCTGTAAATAATAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTCAG
AATGATTTGACGTAAAAGCAAGTCTCATTCAGAAACTGTAAAATCCGTACACACTACTG
AATTTTACATCCATACATTTTTTTTGAATTTTCATGTTTTTTTGAAGAAATGGAAGGGC
TAAATTTATCCGTCGGGGTGTCTCTAGCTCGGCTCAACCTAGGCAAATGCGTTTACTGG
GGCCATCCAAGCTCATCTTCCAGAGATTCGCCTTTTCAGAGGCAAAGAACTCGTCTCCGC
AGGCCTCTTGTTCGGGAGGAGGAGAATTCCTGCGCGGAAACTGGTTGATGCCTGGGCTA
TGGTAATCTGACACCTTTGCTATCCTAAGTGAAGGTCCTTAGTAATAACAATATCA
GGTACTTTAACAATTGTTAAAGATATACTATTAGTGAAGAAACCGATCTTACGAAAGCCAA
TAGAGCAGAAAGTGGTAAAGATGTCTTTAGTTGTACAAGAACAAGGTTCTTCCAACACA
TTTTACGGTATGTTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTACATTACATGG
GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCCTCCGATGGAATAATAAAGC
TCACGGGTACCAAATACGAGGCCGAATTAACCTACGCTACTATAAAAAATTATCACTAG
ATTTTAAAGTAATACACAGTTTATTGGAATAACAATATATGACTCAATGCGAATTTAAA
AATTCAGTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTCTGACGCCA
TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCCTAGCAGTGGTGTGAATAA
ATTACTAACAATAAGATGTACAATTTTTTGTGCGCCCATTAACAATCAGTTTGTGTAACAC
CAATGTCGATGGTAACATTAAAATTGTTTACGCTTTGACCACTATTAAGGGTGTGTCG
TCGTTACTCCAACCTGGTCTGTAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA
ATTGACCCAAGAAGAATTGGAAGAATTGTCCAAATCATGCAAAACCCAACTCATTACAA
GATCCCAGCCTGGTTCTTAAACCGTCAAAACGACATTACTGATGGTAAGGACTACCACAC
TTTGGCTAACCAACGTCGAATCCAAGTTGAGAGATGACTTGGAAAGATTAAAGAAGATCAG
AGCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC
CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208)

MSLVVQEQGSFQHILRLNNTVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLRLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)

TATATTATTTTTTCCCTTCTGGGTTCTTTTCTTCCTTTTCTTGTTTACCTTTTTTGCTTT
TTCATAAAATAATTTCTCTAGATTTGAAGACAGCATTTTTGTACATCCATACACCATACA
CCATACACCATAGCACCAGTACACTATATTTTTATGAATTTTACTAAGAATTATTCCTGC
AGGAGCTCCACTGAAAAAAAAGAGCAGCATGGATGTCCGGTAGAAGTGCTACTGAGTAA
ATGGGAAGGACGCGGTAGATCCAGTGTGGAATCAAGGTGGTGCCGGTGTGAAGCCGCTC
GGCCGGCTGGACTCTCCAGGCCGGAGTGATGATTGCCACGCTGAACGTAACACAGTTTCA
CAATACCAGTGTCTCATTAGTGAGTTCCAATGTATAGTTAGTAGTGGTATTTTGATATA
TGTGAGTGGTAGCAGATTTGAACTTAGTTAGTTGTATTTCGCCTTTGAGGAAACCAAGCAA
AAAACCGATCTAGACTAATCATGGCTGTGTTGTAAGAATAAGAGACTATCCAGAGGTAAGA
AGGGTTTGAAGAAGAAGGTCGTTGACCCATTTACCAGAAAGGAATGGTTCGATATTAAAG

CCCCATCCACTTTTGGAAAACAGAAATGTTGGTAAGACTTTAGTTAACAAGTCCACTGGTT
TGAAGAATGCTTCCGATGCTTTGAAGGGTAGAGTTGTCTGAAGTTTGTGTTGGCTGACTTGC
AAGGTTCTGAAGACCATTCTTTCAGAAAAGGTCAAGTTGAGAGTCGATGAAGTTCAAGGTA
AGAACTTGTTGACCAACTTCCACGGTATGGACTTCACTACCGACAAATTGAGATCAATGG
TCAGAAAATGGCAAACCTTGTATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG
TTTTGAGAATCTTTGCTATTGCCTTCACCAGAAAGCAAGCTAACCAAGTTAAGAGACACT
CTTACGCTCAATCTTCCCACATCAGAGCTATCAGAAAAGTTATTTCTGAAATCTTGACCA
GAGAAGTTCAAACTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAAGTTATCA
ACAAGGAAATCGAAAATGCTACCAAGGACATCTTCCCACTACAAAACATCCACGTTAGAA
AGGTTAAGTTATTGAAACAACCAAAGTTTCGACGTTGGTGCTTTGATGGCTTTGCATGGTG
AAGGTTCCGGTGAAGAAAAGGGTAAGAAGTTTCTGGTTTCAAGGATGAAGTCTTGAA
CTGTGTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKNKRLSRGKKGLKKKVVDPFTRKEWFDIKAPSTFENRNVGKTLVNKSTGLKNASDA
LKGRVVEVCLADLQGSSEHSEKVKLRVDEVQGNLLTNFHGMDFTTDKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVISEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIPLQNIHVRKVLLKQPKFDVGALMALHGEESGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATTGTCTCGAACATGTTACAGGCTCGGAGCTTGTGGCGGGT
GCCTCGCTTACTGGAGTACCATTTAGCGGTGTGTTTGAAGCTAACGAGTTCATCTTCAAT
CTTTATTTCCACTTCTTTACAAGCTTTCTGCCTTTCTCTATGACGCTTTCCCAAACAC
TACCTCTTGACACGACTTGTTGTTTTCTGTTTTCTCTAAGAATATCACTATTTTCACTTT
TTTCACTTTTTCCACCATTACGTCGGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG
GGGAAGAATAAGGGATCTTTGGAACGAAGGAAAATAAGGGAGAGGGAGGAAACAAGGAG
GCGGTGAAAGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCCTAGCATG
ATTAGATTACCGGAGTTTAGAAGAGGATCTGCAATAGAAGAGGAGACAACACTACAAAAGAA
CTGTTAATTAAGAGAAGAAGATGAAGCAATTCAAGTTGGTTAATGCGGTTTCCGCATCAT
TTGTGCTTATTGGCTTAGTGTTGGCCAATTCAGATTCAAGTGTTCGACAAGTGGACGCAGG
AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGAAAAAGTACGCTACAGACT
CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAAC
CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT
TTGGTTATACTGGTTCTTCGGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA
CAGACAGTCTACGTAACCTTCTGAAGAAAAACGGCGTGGATGTTGACGACGCTAAGGCTT
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA
AGTCGTCGGGATACTATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAAGATTTGC
AAAACCTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC
TAGTTTCAGAAAGTCAAGGAAAACATCTACCGAACTTCAGAAAAGGCAGAACAGCAGCGTC
TGGGTTTGCTAGAAAGCTTGGATTGGCTCACCAACAAATATTAGACACATCGGGACAAA
TAAAAGACACTGTATTTGACAAGTGGTCTAGTGATCAGTTAACCAATTGGTTGGAGAGCC
ACAAGGTCAATATTGACAAGAACATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA
AAGAAAATTTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG
AGTCTTCTCCATTTTGGACCAAGACCCAGAAATACGTTGGTTCCGTTTGGGACTCTTCTA
AAAATTTCTCACAATTTGTACTCCAAGTTTCAGAGGTAAGACTGACAATGTGATCAATG
ATACTTTTGGTTGGCCTAGACTCTTGCCCAAAGGACAAATTGAAAATGTTTTTAGATG
CTCGTGATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA
AATCCAGAAACGAAAACTCAAGATCCTGCCAAAAGACTACCAAAAATACTTTGACAAACA
GTAAGTGGTCTTTGGATGACATAAAGGGTGGTTTGTGACAAAAAGGACGACTTCCAAG
ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGACAAGGTTTCCAAAAACACAAATG
ATGCTAAGGACCAAATCGCTAAGACCTGGTCAAATACCTTTCAGAGCTGGTCTCAAGAAG
ACCTATTCAGTACCTAAAATCATTCGGTGTTCGGTTAAACAGACTTCTACGAAGGACG
ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTCCGGCACTGTTAAGGAGCCTG
CTTACAAGAGGTACCTACATAACGTTAAAAACTGGTCGAAAAGCATATTAGGGTTCAACT
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT
EASQVWDKHAQPKPWWQVWSSDSSSVSNSNPGWFGYTGSSDHPVSDWLFDTWSTDLSRNF

LKKNQVDVDDAKASKDSLVTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNLNDN
GIDYDKAVQSKDELVQKVKENIYRTSEKAEQORLGLLESLLDLAHQQILDTSQGQIKDITVFD
KWSSDQLTNWLESHKVNIDKNMAKKHDYLRMAKENSANLKDDIYWYLDYMKRESSPFLT
KTPEYVGSVWDSKKNFLTNLYSKFRGKTDNVINDTFLVGLDSWPKDKLKMFLDARGIKYS
MLSTEHQLRELKKSNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKDDFQDSQTYST
IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFGVPVKQTSTKDDLINLAK
QNTQWLFGTVKEPAYKRYLHNVKNWSKSILGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTTCTTATCTATCTATTTGAGTAATGCTTACTTTTCATATTTTCAATGAAC
AATAGGATATGTAGGAGAATTGATATATTTCACTGCGTATCAGAGAAAAGGTCTACTGACA
TTTTATGGCAAATGTATTCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA
CACAAAGAGAAGACTGTTCTAATTAAACAAATAATATTGAGCTACCTGCTAAGTATGTCC
TTTTCCCTTTGTCTTTGGTTTCTCTTATAGAAGACCCTGGAAATTTTTCGCATTTTTC
GGCTTTGGGCGTTAGTAAGAACAAAAAGAAAAGAAGAGAACAAAAAGAAACGATACGGA
GTACGTGTCATAAAACCTTGTTCAATCATCTTGAAGCTAAGTATAAAGAGCTTGAAAAG
GTTTACCACCTTAAACTGGTTATACTATTTCAAGAGTGTAACATTTTATTGCATATACCA
CAGTAACGTGCAGGTAAAACATGAGATTAGAACCAGCATTTGCCACACTGTGCCCTCACGG
CTTTTACATCTGCACTTCAAACAATAGCTACATCGCCACCGACCAAAACACAAATGCCT
TTAATGACACTCACTTTTGTAAAGGTGACAGGAATGATCAGTTAGTCCCAGTTGTAAACG
TAACATTCATGAATTAAATGCCATAAATGAAAACATTAGAGATGATCTTTTCGGCGTTAT
TAAATCTGATTTCTTCAAATACTTTTCGGCTGGATTTATACAAGCAATGTTTCAATTTGGG
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGGACTGGG
ATACACTGCCCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACAATGA
AGGAAGCGGATGATAGCGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACCAGTA
AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAATGACTTTAACGGTA
AAAACGCCGTTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTATGGTGGTA
AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACCTGTTTTACAATTGGCGAAA
CTGGTGAATCATTTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCCTCTA
TCGGTACTCACTTATCAAAGGAATATTTGAACACGAAAACCTGGTAAATGGGAGCCCAATC
TGGATTTGTTTATGGCAAGAATCGGGAACCTTTCCCTGATAGAGTGACAAACATGTATTTCA
ATTATGCTGTTGTAGCTAAGGCTCTCTGGAAAATTCACCATATTTACCAGAAATTTTCAT
TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAATGGATAACGTTATTTCCAGCTGG
ACACAAAATTTTAAACGAAGACTTAGTTTTCGCAACGACCTAAGTTTGACTTTGAAGG
ACGAATTCAGATCTCGCTTCAAGAATGTCACGAAGATTATGGATTGTGTGCAATGTGATA
GATGTAGATTGTGGGGCAAATTCAAACTACCGGTTACGCAACTGCCTTGAAAATTTTGT
TTGAAATCAACGACGCTGATGAATTCACCAACAACATATTGTTGGTAAGTTAACCAAT
ATGAGTTGATTGCATATTACAGACTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA
ACATGTTGAAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT
TCTTCCAAAATAACTTCTTCAACATTTTGAAGGAGGAGGCAATCGATTTCGTTACACCA
TAGAGAACATCAATTCCACTAAAGAAGGAAAGAAAAGACTAACAAATCTCAATCACATG
TATTTGATGATTTAAAAATGCCCAAAGCAGAAATAGTTCCAAGGCCCTCTAACGGTACAG
TAAATAAATGGAAGAAAGCTTGGAATACTGAAGTTAACAACGTTTGTAGAAGCATTCAGAT
TTATTTATAGAAGCTATTTGGATTTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG
TATACAAATTTTGGAAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG
AGCCTATTTCTTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIALTLCLTAFTSATSNNSYIATDQTONAFNDTHFCKVDRNDHVSFSCNVTFNELN
AINENIRDDLALLKSDFFKYFRLDLYKQCSFWDANDGLCLNRACSVDDVVDWDTLPEYW
QPEILGSFNNDTMKEADDSDECKFLDQLCQTSKKPVDIEDTINYCDVNDNFNGKNAVLID
LTANPERFTGYGGKQAGQIWSITQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNTKTGKWEPLDLFMARIGNFPDRVTNMYFNAYVAKALWKIQPYLPEFSFCDLVNK
EIKNKMNDNISQLDTKIFNEDLVFANDLSLTLKDEFRRFKNVTKIMDCVQCDCRCLWGK
IQTTGYATLAKILFEINDADEFTKQIHVGKLTKEYELIALLOTFGRLSESIESVNMFEKMY
KRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNQS HVFDDLMK
PKAEIVPRPSNGTVNKKWKAWNTEVNNVLEAFRFYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATT
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAATAGCGTCTCTGATAGCCATGGGT
GAAGGTCTTCCTCTAGTTCTCACCTTAATTAGCATTCCGTGAGAATGCCTGCATGTTGAA
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTTGTTCCATTAAATATTATCATC
TCTGATAGAGCTTGAAGAAGTTACCAGACTGTTTCAAGTTTAAAACAAGGCGCCTCATCG
CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT
CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT
AAACTCTGGCGTTTACGCTACGAAGGAGATTATCCTAAAAGGAACTTCCCTAGTAATAGT
GTAATTTGGAAGGGCATAGCATGTCGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC
AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA
TATTCATTTGGGACTGCCTAATTCAAGGGCTCCAGATACGCCATACGCTGATGGTGTTT
TTAATGCTAAGCTAGAGTTTCTTAAAGACTATCCGTTATCTCCACCTAAACTACTTTTCA
CACCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATCTAC
ACTCCCTGGTGATGATCCTAACATGTACGAATTAGCGGAAGAAAGATGGTCCGAGTGC
AAAGTGTAGAAAAAATTCTATTAAGTGTATGAGCATGTTGAGTGAGCCCAATATCGAAA
GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC
AGGTAAAGTTATCCATTTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216)

MSKTAQKRLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPPDTPYADGVFNALKEF
PKDYPLSPPKLFTFPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVKIL
LSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)

GTCTTCCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG
TGTTTTGACAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTACCAGAAGTAC
TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACCAG
AGTAAACACTTCTACCAGTATTTCTTTACGGTTCGGATCAAACCATCACTCATTCGGTC
ATTCTTACCGTACGATAAAACCAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC
ATCCGTAATAGTTTTTTTTTCTATTTTGGACTTTTGTAAAAAAGGGATTAGGGATACGTTG
CTCATAAAAAAATTGACGAAGATTTTAGATAATGGCAAATAAAAATGAAATAGTATCAAT
ATACCGAAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA
TATTTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG
TTCCCGGAGCATCTGTATTTCGTGCAAGAATCAGCACACCATTTATTTTGCATAATTATA
TCTCTAATGGCAGAATGGACCTTTTTCCAAAGAATTCCACAATGGCCGCGTATCCAAAT
CTGATCTTTGGTCAAGCAACAAGGAAGAGGAGCTCTTAGTATCTCAAAGGAAAAAAGAC
CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCTCTTTAC
ATCGTATATCTGGCGTTTTTACTGGCTCTTGGATTCTATGCTTTCACAATTACTTTGGGTG
TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA
AGATGCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTC
ATTTTGTAAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG
GGGTATATAAAAACCGGATCAATCGTTTTCAGCCGGCACACTCGTCTTAGGAACGTATTTAC
TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)

MKATIQRVTSVFGVPRASVFPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN
KEEELLVSQRKRPISPHLTVYEPEMSWYLSSLHRISGVLLALGFYAFTITLGVTTIMGM
DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS
IVLAGTLVLGTYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:
714-1121 (SEQ ID NO 219)

CCGCTTAGCGCAAACCTATCGTGAACCTCGCTGCAACAACCTGAGAGGGCAAGGATATACATA
AAAATAGCCTACAAATTCTGAACTCTGTAAAGGAAGCCTCATAAATAAAGGTAGATAGTA
AAGTATACAAGAGAAGAATCCCAAGATGTCAGCTGTCCCAAGTGTTCAAGTATGTTTTCA
GTTCTCGAGAAATGATGTTTGTATAGTATCGATAATGGAGTGAGATCAAGAGAAAAAATG
AATATGTCAGCCAACCAAGTTCTGAGTAGGCAGTAAATGAGTACGCATAGTGATTTATC
CAAAGGAAAGAATTGTTATTTTTTACAAGCCGAATTGAGATCCAATTAGGCAATGTTTTGG
GGAGAGTATTTTGACAAGATTGGTTAACTACTACGGTCAGTTCCGTAACCAAGTACGATT
GTACACATAAGGAAACAACCTGTAAAGATAAACAATAAGGGCTTCCAATGCCATTGTAAGA

TATCATATTCCCTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTTAAATGGCAAGCGCTACATTTTCATCCATTT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCTCATTTTCTCTCAATGAA
ATAATTGTTACTAACATTGAATTTCCCTCGTAACCTAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTGCCCCATGTCAAGGCCGGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC
CATTATTGTTAGTTGGTTTGGACAAATCTCCAACATCGATATTAGAGTTAGAGTTACTG
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGTTTAGTTG
CTTACCATCAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACCT
CTTACGACAGAACCCTTGTTGATTGCTGATTCTAGAAGACCAGAACCAGAAATTCGGTG
GTAAGGGTGCTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)

MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIAGKLVAYHQKYVDEQSKNELKKAFTSYDRTLIIAD
SRRPEPKKFGGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)

GTCCCATCATTCTTTACACCTCGTACTGTATTTCATGATCATCTATCCATTTTACATACCG
CTCCCTTTAAGATACGTTTATTTCGTAACCTCCCATTTACCAATCACTATGAGCCGTCACG
TTTCCAAAAAACCTAAACATATGATGCAAACTCCAATGAGACTCAACGTAACATGCAA
GTAAATACAGAAGGTTAAGAGATAGTTGCTTTAAAGGGGTACCGAAAGCATTTAGGGGAG
GCTTAAGGGAGGGTGCCGATCCTATGAAGTATTAATACGTAATGCCAAAAGGAATTGTTG
AACATCTGAAGTGGATAGATTAATCGTACAGTAATCGTACAGTACTATGTCTTACTGATG
TCGGGAATCTCAGGGGCGACCGCCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAT
AAAACCTTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTTACA
GCTCAAAGGAAAAATTCAGGGCGATGCAAAAGGTAGTGAGTGACGCTTTTAAGAAAAATGG
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAGTGAAAAACACAACCTATC
AAGAGCAATACAACAAGCTCAAAGGGGCGGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)

MNTDQQKVSEIFQSSKEKLQGDAKVVSDAFKKMASQDKDGKTTDADESEKHNYQEYQYNKL
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)

GGTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT
TCGATGTGGCAGTGACGAGAGCCATTCTGTATCGTTTCGACAAAGTTTGATGACTTCAT
GTTGTTTCGTAGCAGTATTCTGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTTG
TTCTGGTCCACATTTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCTTT
TGTTCCGCTGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCTGTAAAGTCG
CCGTTTCCCTTTAACCATTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCACCATTA
CCGCTTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC
CTTTCCTCTAGCCAATGACTCCAAGCTGGCTGATAAAAAACAACTAAACGGTAAAGCCAC
AAATCCGAAATGTATACCAATGATCACCCAGCTGCTAAGTGCCCTCTATTGATCCGTA
TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTATATGTGCATTGCAAAAGCATAAACA
AATCCTGGCAGCCGAAGCCGGGCAATCCACTTCGAAACGCACGGCTGAACATATATAAATA
TAAAGGACATGTGGAGAGAAGCTTCTCTCCTTCACATTTTCGATTTTCATGATCTAAAGT
GGTTCTTTTACAAATAGAAGAGCACCAACACGAAATATGGCTGTGCGGTGGTAATAACTGGA
GCATGTGGCTGCGAATGTCACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA
CGCTGATCAGTTTGAGCCATGGGAATTTTCCCAACCAATATAATCGCAATATTTTTGTCA
CTTGGTGGAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAAACGG
TATCTCCTCTCACGAGGAGAGGAATCGCAAGGTTTGACCATTTTCAGACCTGTTCCCAATG
TCAGTAAATTTGCTTCTTTTCCAGAGTGCCCAAAGGAGCCCCAAGGGGCCTTTTTACCA
ACTGGAATATGACTACATCAAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA
TCAAATTTTACCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTCAACT
CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT
CTAATGTTACCTCTAAACAGGATCACGTCCAACAGTTGCCCTTAAGAAGTTATCTCAAA
AGGATATCAATTTTCATTCGTAATTTAGAATCTTTAAGATAATGAAGACCCAGAATGAAG
TCGTTGATGAAACAAGCGCATATTACATGGAAAAACCAGGTTCTTATATTGAATTTACCA

TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCATTTTTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAATAATCAATATACA
GTAGTGTGACATGATCTTGCAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTCGAATACATTTTCCAACTCAACTGTGGTGGAACAGAAAACTAATTGCAGGTC
TGAATATGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTAAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)

MITQPAKCP LLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE
ASLP SHFAFHD LK WFFHNRRAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDR TLISL SH
GNFSHQYNRNIFVTWWKSLFEASTAFRRASGLTVSPLTRRG IARFDHFRPVPNVSKFASF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNNMTISLRCFFNSLGG LNQ
CSHSNSCKAYQNASNVTSKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDETS A
YYMEKPGSYIEFTISEFNVNGTFSAPLSFLDPSLLADLDEMIRNYKYELKSIYSSVDMIL
QNYGSLPITFHRNKIRIHFPNSTVVETEKLIALGLNIATGVIYADTSPDISLEGTNLNALV
NVDNSGSVWSFVKEPSFPSRSASFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2:
963-1228 (SEQ ID NO 225)

ATCAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA
GCACTTATTTTTTTTTTGGATTTAGATGTGAGACATACTAAAAAAAGTTGCTATCAAGCC
TATAATTTGGCTACGTTGTCTTCCGGTGTTTTCAATTGATTTAAGTTACAACACTCAAA
TCTGGGTAATTTGATCTTTTTTAATAATTATTTTAGTGACATATAGTTCTTAGAGTTCGC
AGATTTATTTTGTCAATTTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC
ACATCGCGCATGTGTGGGTGATATATGCCCTTTTCACGATTTTTAAGTTGCGTCTCAAAAT
AGTTTCCGAGTTGGAAGCCTGAGTTTTTCAAAACAATATAGGAATTAAGGTATACGTCT
TTGGATACATGTTATTTGAAATGGGGTAGAACTAGCACAACTGAAACCAAGAAAACACAG
ATCATAACTAACCGTTCAAGATGTTGATGCCAAAGCAAGAAAGAAACAAAATTCACCAAT
ACTTGTTCAGGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT
GGATAGCAAAGATGATAAATGAAAATACAATTAAATTGAACTTGAATATCATTAAGGTG
GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCATGAATCCG
AAAGAAAAGTGCACACCTAAGCAGAATTCATTATTTACGCGTCCATTTTTATAAGTGT
GAACTTTTGAGTCCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTTACT
TTACAGTTTCCGGAGTTTCCGTATTATTGCAAAAGGACCACAAACAATTGAAATCATGAT
ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT
AGAAGGTGTTGTCTGCTAAGAAGGATTTCAACCAAGCTAAGCACGAAGAAATTGATAC
CAAGAACTTGATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC
TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTGAG
AGAATACTTGAACCTTGCTGAACACATTGTCCAGGTACCTACATTCAAGAAAGAAACCC
ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)

MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLP EHVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)

CCCTTCGCTAAATCATTAAGAGGTCATTCATGAAGTTAATTCAGCACCAAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTTCAGATAATTGTCGTCGC
ACAAGACTGCCCTCCCGTCCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCCTG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTCGTTCTTCTTATTTCTTTGTT
CTTAGGCATTTCCGCTTTAGAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCTTTCG
ATTTTGCATAATGATCTTCAATTCTACAACATAAAATCAAGTAGATACAGGAAAAATATCC
ATAAATATAGTGATAAATCGCCCTGTATACACCTTATCGTTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAAGCTCACTGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTTATTGTGCAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAAATAGTTG
ATGATTCTGTCGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTTGCCACCA

TAGATAACAATTTAATGGATTCCGATGCCACGTCACATAATCAAGATCATTGGCATTTCAG
ACATAAACAGGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTTAG
AACATATCGGCTCTGTTTCATCAACTAATAATAAGTAACAATGCCCTAATCAACCACA
ACCCTCTGTCTCATCTCATCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT
TGTTGGTAGCTTCTAACCTGCGTTTGCTTCAGATGTTGAACTCTCGAAAGAAGAACCTG
CCGTCATCTCCAATAATATGCCTACAAGTAACATGGCCCTTTATCAAACAGCGAGATCGG
CGAATATTTCATGGTCCATCATCAACTTCCGCATCTAAAGCGTTTCAGAAAGGCTTCGGCCT
TCTCCAATAACACGGCAGCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC
CTCTTTTACCTCTACCTTCACTATCACAACAAAATAAGCCAAAATAATAGAGAGGCCCA
CAATGCACGTCACCTAATTCAAGAGAAATACCTTTTAGGTGAAAACCTGTTAGATGATACAA
AGGCGAAGAATGCTCCCGCAATTCAACCACACAGGATAATGGTCCAGTAGCAATGATG
GGCTGCGTATACCGAATCACTCGAACGCGAGATGATAATGAAAATAACAACAAAATGAAGA
AGAATAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAATATGCA
CTACATCTACTAAAACAGCGCCTTCAACCGCACCTTTGGGCAGTACAGACAATACCTCAGG
CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA
CCAGCAGCAACAACAACGGCAATAACAGTAATAGTGCATCCAATAAAAACCAATGCCGATA
TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTCTAACAAATAATGCAATAAATGACG
ACTCACATGAGAGTAATTTCAGAAAAACCAACAAAGGCGGATTTTTTCGCTGCAAGGCTGG
CTCAGCTGTAGGTGAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG
CAGCTAATTTCGACTAAAAACCTAATATTTCCCTGACTCCTCCAGCCAGCAGCAGCAGC
AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA
GCGCCCCATTGCTAAACAATAACAAAAAATTATTAAGCCGACTGAAAAATTCAAGACATA
TTAGCACTGGTGCCATATTGAATAACACAAATCGCGACTATAAGCACAAATCCGAACTTGA
ATTCTAATGTGATGCAGAACATAACAATCTGATGTCTGGGACACAATCACTGGACGAGT
TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG
TACAATCGGTAGATTTCGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGG
CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACATTTACTTTCATCCA
CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAATTTCGCAGGAATTGG
AACCAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTCTACTTTGAGACATTCCT
CTGCTAATAGAAATTCTAATTATGGTGACAACAAAAGGCTCTTAGAACAACAGTGTCAA
AGATATTTGATTCAAACCTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC
ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG
TGAAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCCTATGGTTTAACTTTT
ATGGTGATAACAAATGTTATTGAAGAGGAAAAATATGGTGACTCGTCTAATGTAATCGAC
CGCAACACACTAACCTTCAGCATGAGTTTATTCAGAAAGATAACGAAAGTGATGAAAACG
ATATTCACCTCCATGTTTTATTATAATCATAAGAACGATTTAGAAACAAAACCGCTAATAT
CCGATTATGGTGAAAGATGAAGACGTAGATGATTATGATCGCCCAAATGCTACTTTCAACA
GTTACTATGGCTCAGCATCCAACACGCACGAACTTCCATTACATGGAAGGATGCCTTCAA
GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT
TGAATGAATATACCCCTTAAGAATGAAAGCTGGTCAAAGACACCTATCAAGAACAACA
ATAGCAATAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCAATA
TCAATAATAACGATATGTTGGTTACTCACCGCACAACTTTTACTCAAGGAAGTCCCCAT
TTGTGAAAGTAAAGAATTTTCTTTATCTTGCAATTTGTTATATCATCACTATTGATGACAG
GATTCATTCCTGGGATTTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG
TGATGGATAATGTGATTTCAAGTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT
TTAATCCAGGATCTTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTGCAAAAA
GTTCTTACCTGAAGTGCGATTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA
TTTTACAAAATAACGACAAATCTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG
GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAACTAGAGACACCATTTAAAGT
TCCAGGGCGGCGCATTTAATAGGAACACGATGTGTCACTCTCGAGTGTCAAGCTTTTAA
GTCTTGGGTCTCGTGAAGCCAAGCACGAAAACGACGATGATGACGATGATGATGGCGACG
ATGGTGACGATGAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAAATGCTAGAG
ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA
TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTCAATACGCAAAAATCTACGGCTA
TTCAAAAGGATTCCATGGTCCATCCTGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVETETVEAPVANNLLSNNSNVVAPNPSIPSASTSTSPHLHREIVDDSVATA
NTTSNVVQHNLPTIDNNLMSDATSHNQDHHWSIDINRAGTSMSTSDIPTDLHLEHIGSVS
STNNNSNNALINHNPLSSHLSNPSSSLRNKSSLLVASNPAFASDVELSKKKPAVISNNM

PTSNIALYQTARSANIHGPSSTSASKAFRKASAFSNNTPSTSNNIGSNTPPAPLLPLPS
 LSQQNKPKI IERPTMHVTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH
 SNADDNENNNKMKKNKNINSCKNERNDTSTKICTTSTKTAPSTAPLGSTDNTQALTASVS
 SSNADNHNKKKTSSNNNGNNSNSASNKTNADIKNSNADLSASTSMNNAINDDSHESNS
 EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSSQQQQQQQPPKQ
 QQQQQNHGITSKISAPLLNNNKLLSRLKNSRHISTGAILNNTIATISTNPNLNSNVMQN
 NNNLMSGHNLDELSSIKQEPHQLQQQQPPMDVQSVDSYTSNDPDSNVIKSPDKRSSL
 VSLSKVSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN
 YGDNKRPLRTTVSKIFDSNPNGAPLRRYSGVPDHVNLEDYIEQPHNYPTMQNSVKKDEFY
 NSRNNKFPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFI PEDNESDENDIHSMFY
 YNHKNDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGRMPSRSNNNDYY
 DFMVGNNTGNNNQLNEYTPLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNNNDIV
 GYSPHNFYSRKSPFVKVKNFLYLAFVISSLLMTGFI LGFLLATNKELOQDVDDVVMNDVIS
 SSDELIFDITVSAFNPGGFFSISVSQVDLDIFAKSSYLKCDSDNGDCTVMEQERKILQITTN
 LSLVEESANNDISGNIETVLLGTAKKLETPKFQGGAFNRNYDVS SVSSVKLLSPGSREA
 KHENDDDDDDDGDDGDDENNTNERQYKSKPNARDDKEDDTKKWKLLIKHDYELIVRGS MK
 YEVPFFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAATTTGGATTACTGCTCCTCTTTTAAGAAGACAAGTG
 TGTGATATCGTAGCGGTAGGAACCAATTTGCAATCGATTTACTTACAGCCAAGAAAATC
 TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTACACGTTGTGCTTGCCAGGAAC TA
 TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGCATCTGATGT
 GTAAACTCATGTGGTGCCTGGTGTGTTTCCAAGACTGCACTATTAAGTGGGAATTTTT
 TTTTTTCTTCTAGTGAATTTTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATATTTTAA
 ACGGACGGCAAACATGAAAAAAAAAATTACCAACCATATTTCTATTTCTTTTCCCTTTTAC
 CTATTTCTTTTGAATAGTTCATTTTCTCTCTCTGAAACGACAATAAACCAAACTCTA
 GCCTCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAACAATTGAAATCCAG
 AAGGTGTTACTGTACGATTAAGTCCAGAATCGTCAAGGTGTGTCGGTCCAAGAGGTACTT
 TGACCAAGAACTTGAAGCATATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
 AGGTTGCTGTTTACAACGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCGTTAAATCTT
 TGGTTGACAAATGATCACTGGTGTACCAAGGGTTACAAGTACAAGATGAGATACGTCT
 ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGTCTAAATTCATTGAAG
 TCAGAAACTTTTGGGTGACAAGAAGATCAGAAACGTCCCAGTTAGAGATGGTGTACTA
 TCGAATTCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG
 TTTCCCAAAATGCCGCTGACTTGCAACAAATCTGTCGTGTTAGAAACAAGGATATCCGTA
 AGTTTTTGGATGGTATCTACGTTTCCCAAGGGTTTCATTGTGCAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTF TKVNNQLIKVAVHNG
 DRKHVAALRTVKS LVDNMITGVTKGYKMYRYVYAHFPI NVNIVEKDGAKFIEVRNFLGD
 KKIRNVFVRDGV TIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVRNKDIRKFLDGIY
 VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAATGGAGATC
 TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAAC
 AGTAATGGAAATGGTAATGATGACACCTCTAATCAGAGAACGGAAGCACTGGGGCGTAAG
 ACGGTAATGGAGGGCGAATATGATTACTAAGTTAAATAAATCAGATACAGTATTTAAAG
 TTCTTTCAAAAAAGATAATGTATATATTTTACTATCTACGCAGTGAAAGAGTTCTCTC
 TAATGACACACTATTTACTTTCGGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT
 TATCCCGGAAATGCGATGAGATGAAAATGCATGAAGTAGCGTATATATTGATTGCATGAG
 GTTGGACTTGAAAGGGCATATATACTCGGTTTATCATTTGATTCAAGTGTTCCTATAAAT
 AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAAATATCTAT
 ACAGAAAAGCGCAAGATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAAC
 AAGCGCTTACGTACAGGGAAGCCATTGCCAAGGAAGTAGCAGAAGATGAGAGTTTACAAA
 AGGATTCTAGATATGACCAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG
 ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC
 GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAGAAATTAAGTCTATTTCCAAATG
 CTGTCAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTAATAAAT

CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACCTCTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCATGCGGGGC
CCAAAAAAGATTCCGAAAGAGTAATCACTTTTGCGAATAGGGGTGATTTTCATTAGCGTTA
GACAGCATGTATATGTGAGAACAAGAGAGGGAGTAGAGATTGCCGAAGTTGGTCCTAGAT
TTGAGATGAGGTTGTTTGAAGTGAAGTTGGGAACCTTTAGAAAAAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLYRKAQELQDSQLQQRQIIKQALAQGKPLPKELAEDESLOKDFRYDQ
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVMVGRHDIINAG
NQSEVNPHLIFDNFTTALGKRVVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVYVR
TREGVEIAEVGPRFEMRLFELRLGTLENKDADVEWQLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:
990-1418 (SEQ ID NO 233)

AAACACCTACTTATAGACACGACCAAACCTTTCCACAACCTTTTCATCAGAGAGAAATGTTG
ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACCTACCTGTCATTCCTGCATAG
TAGTAGTTACGAAAGGCACAGAAAAATAACAAAAAAGTCAATTTCTACGGT
CTCCATCCGTACCTCTTTAAATCCGTACATTATTGTTTTGCTTAATTTCAATATTTTCGGA
AAAAGCGAGCGCCCTGGTAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC
CAAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTTCCAGCCTGGCTTTAGGGAAGAA
TGGGCTCAC TAGGCGTTTATAATACGCGAGGGGGAAATACCAAATGCTATTGATTATGG
TTAAAAATATGTGTTATTTGACTTTGTATATACAAACAGAAGAGAAACCAACACACTAAAG
ACTAGACACATAACTGACCAATGTCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA
GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAAGCTCCTCTCCAGAAC
TAAAGGCTGACTTGAGACCATTGCAAATCAAATCTATCAGAGAAAGTATGTTAAAGTTAT
ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGGTTCTTTGCAGTAATTTTTT
CAAAAAAGAGTGATTTTGGCAGTATCTGTATGAAATTTTCATGTGTTTCGAGAAAAATAG
TAATTCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCT
CCTTGGTCAGTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA
AGGAGAAGAATCACAAACCTTTTTTGTATGAATGAACCAATTCAGTTACTAACTTTAT
TTCAACGCTGCTTGATTCTTATTGTTTAGAATTGATGTACCGGTGGTAAGAAAGCATAG
TCCTTTTTGTCCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAATTTGACCC
GTGAATTTGAAAAGAAATTCCTGACCGTCATGTTATTTTCTTGGCTGAAAGAAGATCT
TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA
CTGCTGTTTACGACAAGGTTTTTGAAGACATGGTTTTTCCCAACTGAAATTGTCCGTAATA
GAGTTAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCCAAGGATG
TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGCTTACAACAAGTTGACTGGCA
AACAAATGTTTTTGAAATTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)

MSSVQSKILSQAPSELELQVAKTFIDLESSPELKADLRPLQIKSIREIDVTGGKKALVL
FVPVPALSAYHKVQTKLTRELEKKFPDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKVLEDMVFPTEIVGKRVRYLVGGNKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:
987-1333 (SEQ ID NO 235)

TTCATCACCAATATAGACTAATGCGTTTTTGGAAACGCCAAACCGCAGTGACAAATAGCAAA
TATGTAGCTGTATATCGGCATATAATAACAGTTTTCTACCAAATGCTGTCTTACATTCA
GAGATCTTACATCCTTACATCTAAAGTAAAACCTAGACATTTACTTCGAGTTATACTTTT
TTTTTATTATCTATTTTTTCTCTTGCGGACATTTTAACACCTGAATTCGCTTAACGCCA
GGACTGATCTGCCAGGGAAGGGAGCTTTGTCTAGTGCCAATAGGCCGGACCACTAGGAA
GGTTACAGCAGCTGGCCCGCAGAGTGATTGGGTACAGGAAATAGCGCAACCTTCTCTTT
TGCCCGGAAAGGCGGTTCAATCTACCTTCGAAGGGCTAGTACATGAGCGCGAAGGAGGC
AGATAATAGCACCATTAAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA
AACAACAATTATCAGTAAAAATGGGTATGTTATAACCATAATTCCTAATGGTGAATAAAA

TCAGGACCAATAAAGAAAAGCTAATTTGATTTTTATTGTCAATGAAATTTTCATAATCGTC
ATGAATGCATAAACAGACACACCTAGCAACTGTATAATCTGCGCCTAAAAAGGGCGTATA
CACAAAACATAACGATGCGCAATAAAAGTTTCAGCAGTCAGCAATGAAACCGAGATATGCA
GCAACAGAGTATCATATGCATGGAGGATCCCTTCTGTTTTTCTGATAATATGCTCTGAAA
AAGCTCCAAACAGCACAGTAGCCTATTTGTGAAGCTCAAAAAAGGCTTCTATTTCCCTCG
CTATCTTTCAGATTGTGCAGTGATATTTCTTTGAGGAAGGAAACGTAGAGGGGATAAGTTGG
ATAACTGTTATTTCTTTTCAATATGCTAGATTTTGTCTTACCACCTTACTGATTTTCTTA
ATAATAAACTTTTTTACTAACATTAGTACGATGTCTCATCTATTTCTTCTATTTAGTTAA
CGTTCCAAAGACCAGAAAGACCTACTGTAAGGGTAAGACCTGTCTGTAAGCACACTCAACA
CAAGGTTACTCAATACAAAGCTGGTAAGGCTTCCTTGTGTTGCCAAGGTAAGAGACGTTA
TGACCGTAAACAATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTCCACAAGAAAGCTAA
GACTACCAAGAAGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACCAGAGCCCAATT
GACCTTGAAGAGATGCAAGCACTTCGAATTGGGTGGTGAAGAAGCAAAAGGGTCAAGC
TTTGCAATTCTGA

YNL162W, 116 aa (SEQ ID NO 236)

MVRCLIFYFYLVNVPKTRKTYCKGKTCRKHTQHKTQYKAGKASLFAQGKRRYDRKQSGF
GGQTKPVFHKAKTTTKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)

GGTCCACGTCAGTTCCACACAATAACATTTACGTAGTGTTCACGCGAAGCAGTTACATCT
CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC
GTTAGTATTTTTGGCCGCCGGTAAATTCCTTGTGTTTTTTTTTCTTGATTTCACTTCTTTT
CATGTTCCTTTGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTGTTCCGT
AACATCCATACCTTTCTGTATAATATCTTGTCTGTAAAGTTTGTGTTTTTTATGAAAAA
AACATTTTCTTTTCTTGAGATGAGGCGCCGCGAGCCTTTCTCCCATGGGCAGTGGTAAAT
TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTCATACATTTTAAGCAATT
TCTAGTTTGTAGATATTGTTAGATTAGTTTGAACATTGTTTTGATAACTGAAAAATAA
ACAGCAAACAACTACAAAAATGGTCGCTTTAATCTCTAAGAAAAGAAAGCTAGTCGCTG
ACGGTGTCTTCTACGCTGAATTGAACGAATTCCTTACCAGAGAATTAGCTGAAGAAGGTT
ACTCCGGTGTGTAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA
GAACTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACCTTGTGTTTC
AAAAGAGATTCAAGTACGCTCCAGGTAATTTGCTTTATATGCTGAAAGAGTTCAAGACC
GTGGTTTGTCCGCTGTGCTCAAGCTGAATCTATGAAATCAAATTGTTGAACGGTTTGG
CTATCAGAAGAGCTGCTTACGGTGTGCTCAGATACGTTATGGAATCTGGTGCTAAGGGTT
GTGAAGTGTGTTGTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAAATTGCTG
ACGGTTTCTTGATTTCACTCTGGTCAACCAGTCAACGACTTCATTGACACTGCTACTAGAC
ACGTCTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA
AGAGCAGAACTGGTCCAAAGGCTTTGCCAGATGCTGTCAACCATCATTGAACCAAAGAAG
AAGAACCAATTCCTTGTCTCATCTGTCAAGGACTACAGACCAGCTGAAGAACTGAAGCTC
AAGCTGAACCAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)

MVALISKRRKLVADGVFYAELNEFFTRELAEEGYSGVEVRVTPTKTEVIIRATRTQDVLG
ENGRRLINELTLLVQKRFKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG
VLGIKVKIMRDPKSRGTGPKALPDAVTIIEPKEEPI LAPSVKDYRPAEETEAQAEFVEA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)

CTTTGATAAATTAATACGGTAAGATACCGTGTGAACCTATTATAATAAAGTCCACGCTTAT
AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT
ATCGTGGAGCATAACTACAACAAAGAATACACAGCGTCACATAGAGGGTTTTTGAGAGGA
GAAGTTGAAATAGGACTTGATCTTGGGGGAGAGGGGATTTGAAAGCACCCATTCAGGAGT
ATGTGTCTGTAATTGAAGTGTTAGCGCGCGATTACCTGTAATAAGAGTGATGATTTGAT
AGCGCCATTCATCATATGGCAAATGTTGAAAACTGTACGCGCGAACTAAAAATTTTT
TTTTACATCCCACTAAATGAAAATTTTAAATCGATGCCATTCCAAATATGCTTATTCGA
AGGACGGCTCTGACAAGGGCATATGCGTTAAGATTGATTGTTCAATATTCAATAAACAGG
ATCTTTCAAGGGACGATAAAATGGATGAGCAAGTTATTTTTACAACAAATACCTCAGGAA
CAATAGCTTCTGTACACTCATTTGAACAGATAAATTTGAGGCAATGCTCCACTCAATCAA
GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTTTATTGCTCAAGCACAAAAAGCAT

TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAAGAGAATCTGTTGAACAGCGCTTAC
CATTACCTGAAATCCTAAAATGTCCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA
GAATTC AAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT
CCACCGAATCGGGTAAATTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA
AGCCTATGGCTCATTACCAAAGTATCACCAAGATTAAGTCCATTTTAAACGGCAAGTATA
TTATTACTTCTGGTAACGATTTCGAGAGTTATTATATGGCAAACCTGTTGACTTGGTATCAG
CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG
ATTTCCAAGTTTCTTCTAGTCAAGGAAAATTTTTATCATGTACTGATACGAACTCTTCA
CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA
AGCAGAAGGCAAACGAAAATGACGTTAGTATTGGTAAGACCCCAGTATTGCTTGCAGCAT
TTACAACCTCCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA
TTGGTACTGCGGAAGGTGTTTTTCATTGAATTTATTTTATAAACTAAAGGGTATGCTA
TCGTTAATCTGCTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC
TAGTGCAACGTAACCTCACTAACTGGCGGCGAAAATGAAGATTTGGATGCATATATGCAA
TGGGCCAACTTGTCTGTGAGAATGTCCTAAATTCAAATGTGTGTCATGCCTAGAAATATCAA
TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTGCGGAAATTT
ACTCAAAACAAATCATTAGAACTATCCAACTTTAACTACATCACAGGATTCAGTTGGAG
AAGTGACCAATCTCTTAACCAACCCCTTACAGACTCGAACGTGGAAATTTACTTTTTGAAG
GAGAATCCAAAGCAAACAACCTAGTAATAATAATGGTCACAATTTTATGAAGATACCAA
ACTTACAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC
AGATAGGAGAACCAGAAGCAGAGACAGATCCTAACCTCGCATTACCACTTAACGACTTTTA
ATGCCTATTTGGAGCAGGTCAAAACGCAAGAATCGATATTTTACATATCGGTAAGGTGT
CAAGCAATGTAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG
CCGCTAAAGATGAGGAAATTACAGAACTTAAGACCAACATAGAAGCATTAACCTCATGCCT
ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA
AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTNTSGTIAVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
SGSFKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
YIWELNSGILLNVKPMAHYQSITKIKSILNGKYIITSGNDSRVIWQTVDLVSASNDPDK
PLCILHDHPTLVDFQVSSSQGKFLSCTDTKLFVTSQDATIRCYDLSLIGSKKKQKANEN
DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKLGNAIVNLLQS
AGVNTVQKGRVSLVQRNSLTGGENEDLDALYAMGQLVCENVLNSNVSCLEISMDGTLILL
IGDTEGKVSIAEIIYSKQIIRTIQTLTTSQDSVGEVTNLLTNPYRLERGNLLFEGESKQKQ
PSNNNGHNFMKIPNLQRVIFDGKNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
KTQESIFSHIGKVSSNVKVIDNKIDATSSLDSNAAKDEEITELKTNI EAL THAYKELRDM
HEKLYEEHQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCCGTACGTACGTAGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCTGTTTGT
TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTTAAGTTTCTTTTACCAATTA
GTGCTCACTTCTCTCGTCTTTTATTAGGTGTGTGTGTTGTGCGTAATTTTCGTTTCGCTG
ATTACTTTATATAGTGTAGTTTGTCTTGAATGTAATAAAGACTTCTGTTTATTTTGT
TTGTTATTTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA
CTACAAGAAAACCAAGCTTCTATTACTTTGTTTCTTCTCTTTTTTCTTTTTTGAATAAA
GAATTTTCTTTAAGGAGTAACTTAAGCATTTAGCTGCACATTAAACACTTTTTTTTTTA
CTTCTAACTCACACACTTTTGAAGAACATTTATTTTTTTCGACCTTCTTTCCCAAATACC
CAGCGCTTTATAATTGAAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG
TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT
CATCGGACGGTAGTTTAACTACTACCACCTCTACTCATACCACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACCCCAAACCACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACTTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACTCCAAACCACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACTTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
ATGCCGCCCTGGTCCATCTAATTTCAACTCCATAAAATTGTTTGGTGTACCGCTGGTA
GTGCTGCCGTAGCCGGTGCCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242)

MKFSSVTAITLATVATVATAKKGEHDFTTTLTLSSDGLTTTTSTHTTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS
NFNSIKLFGVTAGSAVAGALLLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACACATATATATATTTTTCATTTTTTAATGTCTTAGCTTTTGTATCTTAGATGAA
GTTTTAGTTCGTATATCAGCATCAAGATATCATAAATCATAAATTCAATTATCTTCT
GTTTCCCCCTCTTGAGGCATCAAACGAGTGTTTGGCTGATACACACCAACATACTAAGGCA
ACTTTTCTGGCTGCCCAAAGCTGTGGCACGTATGAAACTGCTTTTTCGGCTGCATAAAACA
ACCATGTGGAGTTTTTACTGTATTCGCATTTTCGCCCCGCTAGCATTCTTCGTTTCATGCTA
AAAATGAGGCGTGGGCTAATATTCAATTAATAATTCCGGCACCCGCACAGCCCATACC
GGAAAAGGGCTGGCTGTTGGGCTTGGCAAAAACTCAATCTGAGCAGTCATTTATAAAG
AAAGACTTTAATTTGTCTTGCTAAACACTTGTAAAGCCTTCCAAATATAGATCACTTAAGA
CAATCTAACAAGTGTCCAAAATGTCTGCAACGAATTCCTACTCAAGTGGCCAACAAGGTC
AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGCTCCAAACAACGGTCAATATGGTG
CCGACAATGGTAACCCCAACGGTGAACGTGGTTTATTTTCCACTATTGTAGGTGGCAGTG
CCGGTGCGTACGCTGGATCTAAGGTGTGCAACAACCATTCCTAAGTTGAGTGGTGTGCTGG
GCGCCATAGGTGGTGCATTCTTGGCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC
AACAAGAGCAATACGGCAACTCAAACCTTCGGAGGTGCTCCTCAAGGTGGACCAACAACC
ATCACCGTCAGACAATAACAACAATAACGGTGGATTTGGCGGTCCAGGCGGCCCTGGCGG
TCAAGGTTTCGGAAGACAAGGCCCAAGGATTTGGAGGTCTGGTCCACAAGAGTTTGG
TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTCGGCGGCCAGGTGGC
CAAGGATTCGGTGGTCCAAACCTCAGGAATTCGGGGGCCAAGGTCGTCAAGGATTCAT
GGCGGTTACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGQQGQYNQNNQERTGAPNNGQYGADNGNPNNGERGLFSTIVGGSAGAYAGS
KVSNNHSLSGVLGAIGGAFLANKISDERKEHKQQEQYGNNSNFGGAPQGGHNNHHRQTIT
TITVDLAVQAALAVKVEDKAHKDLEVLVHKSILVQVAKDSVVQILKNSAARWPRIWRSK
PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTTCTTTTCAAAAAACCGTAAAAATTTGAGGTCACACCAACTAAATACAAA
TTGTTTCATCAGCGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACTCAATA
TAGTAAAGTTTCATCAGCAATCTTATCTGAGTAATATTATCTACGATCTAAATATAGGAT
GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC
CTTTTACAAAGTGGATACAGGTTGCCTATCACTACCGCCATTTCACTAGCAAGTAGAGTA
TTGAGAAAAACGGTAAACTTTGAAAGTTGCAGATGCAGAATATATATCTGGTTTTGTAGTT
CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTTAATATAAGTAATGAA
CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTAAATC
AGCTAGTGCATACCAAAACAATGAGTAACCAACACAGCCCTCAGCCATTTTGTGTTGGACA
CCAAATTGGTGAAACTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCAACAATAAAAAACA
TATTCCCGGAAAAAGCATTATATTTGAAGCTCGCTCTTGATTATTCTTTCTCAGAAAGA
ATTTACTAGAGTTTTGCGTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG
ACACTATATATATTTTGTGCCTGTTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA
ATATATTGGAAATATGTTTGGCCAGGTTTGTTCAGGGAGGACTTGAGGGTTTTTAATA
ATACTTTTACACATATCAGGATAACCGCTACGTATTCTCCAAGAAGACTTTCTCAAT
TGTTCAAAAAAATCAAAACTAAGGCTTCTGTACTATGTTTTACAGTTGAGGAAATTTTTT
TGACAAACCAAGAAATTTTACCTCAAAACTCAACAGTGGCAGAACTGCAAAAAGACACTA
ATAAAGTACAGACAAATGGGCCGCAACGGCACGATTTTCATAGTCACTCTAGAAATAAAAC
TGAACAAACACAAATCACTTTCCTCATTTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA
GGGAAAAATCAGGCGCCAGCATAAAAATAATACCTATTAGTGATAAAATGACTGCACATG
AAAGGAACCACCTGAATCTGTTCAACAAACAATACTAATTTCCGGTGACTTACTCTAA
TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTTATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPQPFCLDTKLVLLEELQEGKQFNKNIFPEKALYKLALDYSFFRKNLLEFCV
HLDKIKGVIRPNYDTIYILCLLEVDLLNLVFTDNILEICLPRFVSREDLRVFNNTFYTYH

DNRLRLIQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNQ
PQRHDFIVTLEIKLNKTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPE
VQQTILISGDLYSIALAVTSIESALITLDEL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTTCTCGAGAAATTGTGAACAAAAGCAAAGACACAGAAAGATGATAAGAG
AGAGAAACAACGAAGAAAGAACAACAATGTTGGGGTTACCCGAGAGATATTGACATACT
GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA
TATTTCTTGTTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA
TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAAGTGTCTGGA
CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCCGGTAACGGAA
TTGTGATAATTAAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA
TTAGCAACTATAATAGACTAGTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT
TCCAAGAACGCAAACTTAGAATGGTCCGGATTCTTCCATAATTTTGAGCGCCCTATCTT
CGAAATTAGTGGCGAGTACAATATTGCATTCATCCATACACTCAGTGCCATCTGGAGGCG
AAATCATATCTGCAGAAGATCTTAAAGAACTTGAAATTTTCAGGGAATTCGATCTGCGTTG
ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATCTGCCAG
GTCAAGAACTCCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAAGAGG
CAAACTAAATGATGAGAAGAATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT
CAGAAGACATGAAAGCATCGCCTGGTGACTATGAATTTTCCAGTGATTTCAAAGAAATGA
GAAACATCATAGATTCTAACCCGACTTTATCTTTCACAGGACATTGCCAGATTGGAGGATA
GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC
ATGAATTCGCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG
AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAACAATCCTCCTGTAGTCGAGTTCA
TTAATGAAAGTTTCCAAATTTTAAAAGCAAAATCATGGCCGCTCTGTCAAATTTGAATG
ATTCTAACACAGATCCTCTAATATCCTAATAAAAAGATACTTGTCCATTTTAAACGAAT
TACCTGTCACATCCGAAGATCTTCTATATACTCTACGGTTGTTTTACAAAATGTATATG
AAAGAAACAACAAGGACAAACAGTTACAAATAAAAAGTCCTGGAGTTGATCAGCAAAATTT
TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAAGAAATGCTG
AGAATTGGTTCGTCAAATCTGCAAGAGTGGGCAAACGAGTTCCAAGAGATGGTCCAGAACA
AAAGTATAGATGAACTACATACAAGAACGTTTTTTGACACCCTTTACAACCTGAAGAAAA
TTTTCAAAAGTGACATCAGATCAACAAAGGGTTTTTGAATTGGTTAGCGCAACAATGTA
AAGCCAGGCAATCTAACTTGGACAATGGGCTCCAAGAGAGAGATACTGAACAAGACTCAT
TTGATAAGAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA
TAAAAAATTTTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSSKLVASTITLHSSIHSVPSGGEIISAEDLKELEISGNSICVDNRCYPK
IFEPHRDWQPIILPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS
PGDYEFSSDFKEMRNIIDSNP TLSSQDIARLEDSFDRIMEFAHDYKHGYKII THEFALLA
NLSLNLNLPLTLRELSTRVITSLRNNPPVVEFINESFPNFKSKIMAALSNLNDNSNHRSS
NILIKRYSILNELPVTSEDLPYSTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFDLYNLKKIFKSDIT
INKGFLNLWLAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAAGTACATGATTTTTGTTTGCATTGATATGACTTGTTTTATGACTAACATATTTAATTT
TTATTTGTTAACCGTAGGGGTTTTATGAAGTGCTGACGAATCCTGTTTATTGGAAGCATA
TTTTACTGTTTGC GGTTTGCTATGCCCTGATTTTTGTCACTATTGCTGGTCTCTTTATG
TCACACTTGTACCGCTTTTAGTGACATGGGCCATACGTATTATTAGGGCCTCTTGGTGTGA
TACTGGTTTCATATTC AATGGATTTTACAAACGAATGTCTTGACTGCCTTTGTTGTAGAA
CACTGGTTCCTGACCCATATTACGAATCAGATATTTGATATATCTTTGGTGTTCGAAGACC
AAGATGAATTTCTAAACGAGGTGAAGGTATTGCC TAAACCACAAAAGCCACATAGAAAAA
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGAAGTCGGATTTTAAAGA
TTCCAGATTACTATTTCAGAATGTTTTTAAAGTCTCCAATTTTACTTCACTAACATTAC
TGTCGCTAATTCCTATTGTAGGACCAATCTTGGCAAATCAACTAATGGCCCCAAAAAGAA
CCTTTACCTATTTGCAGAGGTACTTTTTACTAAAGGGATTTCAGTAAGAAAACAGGCCAAAG
ATTTTCAGTACGAGCATTACGCAAGTTTCATATGTTTCGGTATGTCTGCCGGTCTACTAG
AGTTAATACCTTCTTCACAATAGTCACCATATCTAGCAACACTGTTGGTGCAGCTAAAT

GGTGTACTTCGCTACTAAAGGGTGAAAGAAAGAAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFFKVSNFTSLTLLSLIPVGPILANQLMAPKRTFTYLQRYFLLKGFSSKKQAKDFQYEHY
ASFICFGMSAGLLELIPFFFTIVTISSTNVGAAGKCTSLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)

ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCTTGGAGGAAT
CATAGGCAAAGAAAGAAAAGAAGTTCATCTTTAAACTACCTTTCAAGCCTTTATTC
GTTCCCTCGTAAAGGACACACGAAAAAAATAAACAGTACCTTGCAGAAAGGAGTGACAGATT
AGGTCGACAGGAATCCTTGAAAGCCAAGAGTTTTTTTTTCCGTAATGATCTCCCAAAGCAA
CCATCAACATTTGTGGTGCAAGTTTAGTGTAAGATGTTCTACTGAACTATCTTAATAGCT
GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAACAACAAAGTAATGTTCAACTTTCGTA
ACTACGGAAAATAATATATAAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT
CATCTTCTTTTCCAGTTTAGCCATTATCAGCACAAATAACAAAACACACTCGTACACTC
GCTTCAACTATAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG
CTTTGGCTTCTGCCCAAACCTCAGGAAGAAAATTGACGAATTGAACGTTATTTTGATGACG
TTAAGTCCAACCTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT
TAAGCAGTCTGCCATCTGGTGTTTTAGACATCGGTTTAGCTTTGGCTTCCGCCACTGATG
ACTCCTACACTACTTTGTACTCTGAGGTGACTTTGCTGCTGTTAGCAAGATTTTGACCA
TGGTTCCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACCTCTA
CCACCGCTGCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCT
CCAGTGAACCTACTTCTTCTGCCGTCGCTTCTTCCAGTGAAGCTACTTCTTCTGCCGTCG
CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGCTGCTTCTTCCAGTG
AGGCTACCTCTTCCACCGTCGCTTCTTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT
CCTCTGCTGTTTCTTCAAGCTGTTGCTTCTTCCACCAAGCCTCCGCCATTTCTCAAATCA
GTGATGCTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAAACTGAAAACGGTGCTGCCA
AGGCTGTCATCGGTATGGGTGCTGGTGTCATGGCCGCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)

MAYIKIALLAIAALASAQTQEEIDELNVILNDVKSNLQEYISLAEDSSSGFSLSSLP
VLDIGLALASATDDSYTTLYSEVDFAAVSKMLTMVPWYSSRLLPELESLLGTSTTAASST
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSAATSSAVASSSEATSSSTV
ASSTKAASSTKASSAVSSAVASSTKASALSQISDGQVQATSTVSEQTENGAAKAVIGMG
AGVMAAAAML

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)

CATTGATCTCGAGCACAGCTGCTCTTTTCTCTCAATGAATTACGTTATATGTTAATCACA
CAAGCATCAGTTTTTTCATCGCAAAAGAAAATATTTAGAGTTCTTGCAATTCAGATGTACC
TCAATTAATAACTCAATCACCTCCTATGTTCTTGCTGGTAGTACTGCTTTTGTCTTAATT
ACTGCTGAATCAGCCTTCTAGAAGACCGTCTGTTTCAGCCGCTCGCCCCCTTTCAAAGC
TTGCGCGGCTGAGTTTTATGAGGGGCGGCTTTTGTGTAATGGCAATCTACCATTATTAG
TAGCAATATGATTTGCAGATAGATACATATATATCCTTCTGGGTTCATGTCTCGTTACCA
TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAAAATAA
GGACTCCTCATTTAAAAGGCTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG
CAAGTCAACCTTAAATTATTATGATTTCTGTTTGCCCAAAAATGACTTGCAAAAATGCT
ACAGAAGCCTCACATTCGATGTTCCAGGACAACAATTCGAAGAGAGAAATGAACAAAACC
TTAAAAAACGGGCCAAAAGAAAGGCAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC
CTTCCACCGCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG
TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTTCGCCAA
ATTTGCAATATTATTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG
AGAACAAATCTGAATCCAGTAGTTTTCCAATGAGATCCTCAAAGTTGTTGGAAGAAGATT
CTGACATCAAAAATATTTCTTGGTATCCAAGAAATGGAAAATAGTGAGGAGAGACTATC
CAAGCACGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAAAGAAGTGGGA
TAAAGTTATGGCGCCAAAGAAAACCTACAAATAATGAAAGGCTGAATGACAAAAAAAT
GGTTTACTTACCAGAACTTATCTTCTGTAAGAGCGTATTAAACCGTTATATAGAGGAG
ATGATAGTGCACCATGTACAAAAGAACAAAAAGAAAGCATAAAATACTTCAACAAAAGG
TCGGATATCCCAATAACCCTAAGACAATAGTTTGTACATTAACGGAAAAAACATACGT
GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA
TAACTACACTGCCAAAATGATTTCTAACAGGAAAAAACTGCAAAAGATGATACAGAAAT

GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTGTGATTATA
TTTTACAGCTAGTAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAAATAATTGTAG
GCAAAATTAAAAAAAGTCTGGTAGATGTCATTAATGTCCATACTCCAGATTTCTTAGTTTC
TTGCTACTTTAAAGCACGAGCGAAATGAGAATCTTATTACATATAAAATCCAAAAAGCTGA
CAGATGCTCTTTCCTGTTAGTTATCCGATTCCCACATTTGTTGTTCCCTCGAAACGAATGT
ATTCTGTTTCAAACTGAATCTACAAAGAGAAGTAAATGAACATTATGTCTCAAAAAATCATA
TGAAGCACGAACACACTGACGTGAGAGCATGAGCAGTTCAATGTTCAAAAAAATACAA
TATCAGATATTTCTTCACATATTTCCGTAGATTTCGTACGCCGAAGATTTCAAAAGGCAAG
GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAATTGACCGGTC
TCGCCACGATTTCAAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA
AAGATAGAGAATGTACTAAGGAAAAACTTTTGTGTTGAAGAAAATTGATATCATAATTAGAG
AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA
CTACGGTGACCAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTCGAAAAACA
CAAAGTTTAGAAAAATCTTTAATACCATATCTTCCCTCAGAGGAACAAAATACCACAACAA
CTATTAAACTCAGTAGCTCGCCTACGTCCCAAATCAAGTTTGCAACCTCTGTAAAAACACA
AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT
CCTTCGACAAAGAAAATTCTTTGATCCATCTGATAAAAGCAGTAGTGTGATAATAGCA
TTCTTTTGAGGAAAGTTAAAAAGTGCCGGTGCGTTAAGAAAAGTCAAACTAATGACTCCT
CAAGTAGTGCAGGGTCAAAGAAAAGCTCGTCTAGTTTGTAGTACTGTGAACACCTTCACTG
GGGTGAGTTGGGATTTTAAAGGTGTTTAAAGTGGAAGTTCTCTGGAAATAAATCAT
CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTTTGAAGTGATGATCGTAACGACAAGA
AAAAGAAGAAGAAAAAAGAAGAAATCATTGTCTTATTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQQFEERNEQNKKRAKKKGSFQPSVAFDTPVSTAGYS
SIDDSREGFKGVFPVNYTMEECYDDETDSEFSPNLQYYLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLLKNSDIKKYFLVSKNGKIVRRDYPSTPVIIVNETLMINRFEKNWIKLWRQR
KLQINERLNDKKKWFYTPELIFSEERIKPLRYRGDDAPCTKEQKRKHILQQKVGYPNNP
KTIVCHINGKKHTWVALDWTVYKFARNLDHIVVITTLPKMISNRKKTAKDDTEWAPGYQK
EVIDQKLNDFDYILQLVKVVKISVKITLEIIVGKIKKSLVDVINVHTPDLVLATLKHE
RNENLITYKSKKLTDFVPVSYPIPTFVVP SKRMYSEFELNLQREVNEHYVSKNHMKHEHTD
VESMSSSMFKKNTISDISSHISVDSYAEDFKRQGYIKKQFNTSND SI PRKLTGLAQHSRR
KITGDI EKLQDDEK DRECTKEKLLKKIDII IRESL KSSLAIETLP GKNVSQSSSHGDQIS
SFKNALIGNSKNTKFRKSLIPYSSSEEQNTTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFDPSDKSSSVDNSIPLRKVKSAGALRKVKTNDSSSSAGSK
KSSSSSFSTVNTFTGGVGIFKVFKSGSSSGNKSSSRNSSSGDVFESDDRNDKKKKKKKK
KKSLFLFGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AATTTTCCCCCGTCATAAGTTCTTATACACGGCTGGCTCTGATGGCATAATTTTCATGCT
GGAACCTACAAACCCGCAAGAAAATAAAAAATTTTCGCCAAATTTAACGAAGACAGCGTGG
TTAAAAATTGCTTGTTCGGACAATATTCTATGTCTGGCAACTTCTGATGATACTTTCAAGA
CAAACGCGCAATTGACCAAACATATTGAACATAACGCAAGTTCAATATACATAATATTTTG
ACTATGAGAACTGATATCTTCGTGAAGATTCTGTGTAGTATGATAGAACATTCAGAAAAA
AAATTCAGATTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAAATCA
CATACATAGATTAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATCAATCATCTTA
TTAAGGTATCTTGTTTAAGCCCCAAAAGTCTGCTCCCAAATTCCTCACTGTAGCTACTAAA
ACAACCTATACGCAAGAAAGATGTCATTGACAGCCGATGAATACAAACAACAAGGTAACG
CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAAG
TTTCTGAAACTCCAAACCATGTTTATATTCTAACAGGTCCGCTGTTATACCTCTTTAA
AGAAATTTAGTGACGCATTGAATGATGCTAATGAATGTGTCAAAATCAATCCATCTTGGT
CTAAGGGTTATAATAGACTCGGTGCCGCCCACTTAGGTCTTGGCGATCTCGACGAAGCTG
AAAGCAACTACAAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCCAAAGAAGGAT
TGGATCAGGTTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC
AGTTGTTTGTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCCAAAAACTAGCGAAA
TGATGAAGGACCTCAATTAGTGGCTAAACTGATTGGGTACAAACAAAATCCGCAAGCTA
TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATGATGGGGG
TTGATTTAAACATGGATGATATAAAACCAATCAAACCTCCATGCCAAAGGAACCGAAACCA
GTAAGCACTGAACAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG
AAAATTCCTCTAAAGCACACAGAAAGAAGAAAGTAAGGAATCCGAGCCAATGGAAGTTG

ATGAAGATGACTCTAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTTTACA
AGGCACGTC AATTTCGATGAAGCTATAGAGCACTACAACAAGGCGTGGGAACTGCATAAAG
ATATTACCTATTTAAACAACCGTGCTGCTGCTGAATACGAAAAAGGCCAATACGAGACAG
CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG
TCATTTCCAAATCATTGCGCGTATTGGTAATGCCTATCACAAATTGGGTGACTTGAAGA
AACTATAGAATACTACCAAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA
AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCCTG
AAAAGGCCGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA
ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTAGAGGATATT
CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTTCCCTGAAGCTATCGCAGATTGTA
ACAAAGCCATTGAAAAAGATCCAAATTTCTGTGAGAGCTTATATCAGAAAGGCCACCGCAC
AAATTGCTGTTAAAGAATATGCTTCCGCTTTGGAAACACTAGATGCGGCCAGAACCAAAG
ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGGAATTGATCAACTGTACTACAAAGCAA
GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCAGAAGAAACCTATCAAAGGG
CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAGTATTTTGC
AGCAGGCCCAACAGAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA
AAAAGATTTCAGACGTTGATCGCTGCTGGTATCATCCGACTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTAD EYKQ QGNAAFTAKDYDKAIELFTKAI EVSETPNHVLYSNRSACYTSLKKFSDAL
NDANECVKINPSWSKGYNRLGAAHLGLGDLDEAESNYKKALELDASNKAKEGLDQVHRT
QQARQAQPD LGLTQLFADPNLIENLKKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT
DPR LMTIMATLMGVDLNMDDINQSN SMPKEPETS KSTEQKKDAEPQSDSTTSKENS SKAP
QKEESKESEPM EVD EDDSKIEADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN
RAAAEY EKGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTIEYYQ
KSLTEHRTADILTKLRNAEKELKKAEEAYVNPEKAE EARLEGKEYFTKSDWPNAV KAYT
EMIKRAPEDARGYSNR AAALAKLSFPEAIADCNKAI EKDPNFVRAYIRKATAQIAVKEY
ASALETLDAARTKDAEVNNGSSAREIDQLYYKASQQRFPGTSNETPEETYQ RAMKDP EV
AAIMQDPVMQSILQQAQQNPAALQEHMKNPEVFKKIQTLLAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAGTACAGCTGCCTTTATTTCTTGTGGTCATTTATTGCTTTTATTTTCAAGTCA
GATATACAAGAAAATCAAATCCCATCGTCAACGTCAGTATAAACGATTAATTTACAGTA
ATACCATACTCTACCAACATTATTTTAGTCCGACGTTCACTCTGAGGTGTTCCAAATC
CTTCTGGCATTGACTTCTGTGCGAGAAACCTTCAAAATGAGTTCCACTTTTCACTGATC
GCATAACAACCGGTCATATATTTTTTTCTTTTGCTAAACCCCTACTGCAAGCAC'TTTTA
AGAAAAAGAACAATAAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTGTCTTTTCGGAC
AAAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCCTATATAAG
AAGGGCGCACATCGTCCCCCTAAGAATAGCGAAGCGATATTACACTGAACACTACAATG
TCAAAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA
AGGACTCTTGTCAATTGTGGGAGCACCTGCC'TTCCAAGCTGTTCTGGCGGTGAAAAGTGCA
AATGTGATCACAGCACCGGAAGCCCTCAATGTAAGAGTTGTGGTGAAAAATGCAAATGCG
AAACCACGTGCAC'TTGTGAAAAGAGTAAATGCAATTGTGAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECKD SCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE
KSKCNCEK

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:
1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCCAAACATATGATATGGTATTAAAAAATGAA
AAAAATTCATTATTCTTTAGCGTAATTATTTGAAGAAAAAACAGTGC GCGCGGTAATTTTT
TGTCACCTCAGTAAC TAGAGAGAAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC
TCTGCCTAGGATTTCTCTTATGCTTTCC'TTTCACCAATCACTTTGTTCCGGCGAGGCCCG
CGAAGCTCGCTTTCTTTACGCCTAGCAATCATGTTCTTGCCAGCGTCGTAGACTACTGTA
TGGCAGTTGCTGCACTTGCCATGAATATCCTAGTGAAGCCTCTATGCAATAATCCAGTTA
CTGCGTTAGAATCCTGGTAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT
TGATTGAAAATTAGTCCTTGCGACTTGGTATATATCTTATTTTAAGAAAGCTGAAAGGAA
GAAAGATCATCACGAACAACATGTCTGCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA
CTGAATTGGAATTACAAGTTGCTCAAGCTTTTCGTTGAATTGGAAAATTTCTTCTCCAGAAT

TGAAAGCTGAGTTGAGACCTTTGCAATTCAAGTCCATCAGAGAAGTATGTTATTAATTTG
AATCTAAACTTAAGAATAATGGAGAGTAACAAAGGAAAAAGTGTGAACGGGACGATACC
AGAATGTTTCAATCTAGAAAAGTATAAAAGATAAGGACTAGGACTCAAATGTATTTGGCT
GACTATCGCCTGAACCTTGATGCTAAGCAAATACCATATCTTCAAGAAAAAGCCTACTCC
AGTGTTTAAGAAGAAGGGAACGATTTACTAGATCATGCTATACGCAGTAAGGTTCTGATA
GTTAATTACAATCGGTCCAAGTTCTAAGCGGTGTCGTCCATGCATATATCATTTACAAGT
TACTGGCGTCAACTCTTCAAATATTCAAAATATCACCTAATCAAACCTACTAACATTTTC
CTTTTTTGTCTTCTCTTTTATAGATCGACGTTGCTGGTGGTAAGAAGGCTTTGGCCAT
TTTGTTCAGTCCCATCTTTGGCTGGTTTCCACAAGGTTCAAACCTAAGTTGACCCGTGA
ATTGGAAGAAATTCCAAGACCGTCATGTCATCTTCTTGGCTGAAAGAAAGATCTTGCC
AAAGCCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACCTTGACTGC
TGTTTCATGCAAGATCTTGGAAGACTTAGTCTTCCCAACTGAAATCGTTGGTAAGAGAGT
TAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCAAAGGATGTCCA
ACAAATCGACTACAAATTGGAATCTTTCCAAGCTGTTTACAACAAATTGACTGGTAAGCA
AATTGTTTTCGAAATTCCAAGTGAACTCATTAG

YOR096W, 190 aa (SEQ ID NO 260)

MSAPQAKILSQAPTELELQVAQAFVELENSPELKAE LRPLQFKSIREIDVAGGKKALAI
FVPVPSLAGFHKVQTKLTRELEKKFQDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKILEDLVFPTEIVGKRVRYLVGNGKIQKVL LSKDVQIDYKLESFQAVYNKLTGKQ
IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)

ACCCATTTTACAAATTTTTTTTGTATTTGAGCCATAGTACCCATTAATAGGTCTCGTCC
ATTCCTTTGTTTTTTTTTTTATTGTTTCAATTACACTACATAATTAATAATCACATCACTT
TCACCTGCACCTTAGTCGTTCTTTATCAACCAAAAATAAAAAATGCTTCAATCCGTTGT
CTTTTTTCGCTCTTTTAACCTTCGCAAGTTCTGTGTGTCAGCGATTATTCAAACAATACTGT
TTCTACAACCTACCCTTTAGCGCCAGCTACTCCTTGGTGCCCCAAGAGACTACCATATC
GTACGCCGACGACACCACTACCTTTTTTGTACCTCAACGGTCTACTCCACGAGCTGGTT
CACCTCAACTTCAGCCACCATTACCAATGCGGCCTCCTCCTTGTCCACCTCTTCGGC
CTCTGGATCTGTAACCCCAAGATCCACCCATGAAATTACCTCCACCTCGACTATCACGTC
CACTTTGCTGCTAACCTTTCATGACTCCACTACTTTGTCTCCATCATCTACTGCAGCAAG
TGTCAGTGGAAGATTCAAACAACAAGATGCAAAGGTCAAGTCCTTTGAACAGGCTTC
AACTTCCAATGGTTGCGTCCCAATCACAAAGTTTGTCACTGTCAACCAATGAGCCGTTAC
CCAGTACGTTACAGTACCCCAATACTGACTACACAATACGTTACTGTACCCGGTGCACC
TTCTGTTACCACTACCTCTCCAGGTAACGTACAATGGTACAACACCACTTCGATTACTAA
TTCGACCAGTTGGTGAATTATGA

YOR248W, 100 aa (SEQ ID NO 262)

MTPLLCLHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSLSLSPMSPLPSTLQSP
QIRLHNTLLSPVHLLPLPLQVTYNGTTPRLRLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:
990-1255 (SEQ ID NO 263)

AACTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCCCTAATGCA
AACACACGTCCTTTAAAGATCCCTGATAGGTTTCATTAAAGGCAACTTCCATACACGTT
GAAGTGCCAATTTTTTCCCTACATCCAAGCATTTCTGGGTTTGTATGGGTGTTACACCGGT
TTTTCTTTTTTATTTCCAGAGAAGTACAATTTTAGGCGGGTTCAAATTTCCCTGTGTG
CGAGAAAACGCTCCGGTACGCCTAGGCTCACTCCGGTCTTCTCCCCATTTCTATCAGCGC
GATAGGCATACTGTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA
ACGCACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACCTTAGATTAACACTGGTAT
TAAGATTTTCGCAATTTTGGGCTGGATTATTAAGGTCGAGTAGCAAAGTTTAGCAAAGAACA
GTACGAACTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT
ACTTATTCCAAGGTATGTTTTAGAATAACTTTTCAGAAAGCATGAAGATACACGGAAAGTC
AAGCGAGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGCATTACATACAGATGTT
TCAAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA
AGGCCATCGACCCTGGAGACGTATGAAATATGGTATACGTCCTATATTTGGGCAAGAAAA

CGGTAAAACTGTTTTACGCGGAGATCCAACTTTTGATCCTTACCGAGTACCACGAATCAT
CTATATGATCTTTTTACTAACTTATCTTCAATTTCAACGGAGAGATGTAAACATCATTTCT
CTCCTATGATAATTTCTTTTTTATACAGAAGGTGTTGTTGTGCGCCAAGAAGGATTTCAA
CCAAGCCAAGCACGAAGAAATTGACACCAAGAACTTGTATGTCATTAAGGCTTTACAATC
CTTGACTTCTAAGGGTTACGTCAAGACTCAATTCATGGCAATACTACTACTACACCTT
GACTGAAGAAGGTGTTGAATACTTGAGAGAATACTTGAACCTGCCAGAACACATTTGTTCC
AGGTACCTACATTCAAGAAAGAAACCAACTCAAAGACCACAAAGAAGATATTAA

YOR293W, 105 aa (SEQ ID NO 264)

MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLEPHIVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:
915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTCATATCTTAAGGT
GCTGATTGTTTTGTAGGCACGAAGTAAACAAGCTCTTCCCCAAAACAATAAATACGGTTTTT
CGGGACTGTTCAACCGTACATTTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTTTT
ATCTCTTTTCAGGTAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC
CGGGCTTAGACAGTTACTTCCCAGGCCAGGGCCAGGCCACACGGACAGAGGCAGATTCCA
AGTTGATTCGCGATAGTCTGTCTAGCTCTTTCTCAATTTCCGCCAGATTCTGTCTAATTT
CTTCCGCTCGAGTTGGCAACAGTACGAAGAAGTAACTCTAATAGATAGATAAACCCTT
TTTGAGGGCATTATTTTTGCAGAAGATAATAGAAGAGAACCCTAACAAGGAATCAAGCA
AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT
TTTATATGGTGAGCTCAAATTGAATGAACATATCGTGGAATTTAAAATACTGAAGAATA
CCCAATAAGTCAATGCAACCTGTGAATGTTTTTCCCTGAAATACGCCGAATACTGAATACG
ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATATG
GTTAATATCATTTGAGAAGTCTTACATGAGGACTATAGAATACTACCATCCAGGAATTATA
GAGGAAATTAACGTAATCAGAGATCTATTTTGAAACATTCAATTTACATGTAATTGCTCTGC
AATAAAGCAATATTTTTGAAATATGCAAGTTTACTAACAAGAATAAATTTCTTTTTTGATT
TTTATCTTTAACAGTGGCTCATTTCAAAGAATACCAAGTCATTGGTCTGCTTTACCAAC
TGAATCCGTTCCAGAACCAGGTTGTTTCAAGATGAGAATTTTTGCTTCAAATGAAGTCAT
CGCCAAGTCTCGTTACTGGTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG
TGAAATTGTTTTCCATCAACCAAAATCAACGAAGCTCACCAACCAAGGTCAAGAAGCTTCGG
TGTTTGGGTTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGA
CGTATCCAGATTGCTGCGTGCAGAACCTTTTACCAAGACATGGCTGCTAGACACAGGC
TAGATTTAGATCTATTCACATCTTGAAGGTTGCTGAAATTGAAAAGACTGCTGATGTCAA
GAGACAATACGTCAAGCAATTTTGACCAAGGATTTAAAATTCCCATTACCTCACAGAGT
CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)

MYLAHFKEYQVIGRRLPTESVPEPKLFRMRIFASNEVIKSRWYFLQKLHKVKKASGEI
VSLNQINEAHPKVKNFVWVRYDSRSGTHNMYKEIRDVSRVAAVETLYQDMAARHRARF
RSIHILKVAEIEKTADVQRQYVKQFLTKDLKFPLPHRVQKSTKTFYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAATAGTATATATATGTAAAAAAATTTCTGCTTCATGTATATA
CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT
ACATCTTGGCATATTAAATGGTTATTTTCGGGGTTTGTTCGGCTCAACGGTGATATAAAA
AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTGTTTACAACATCTTC
ACATTTCCATTGTGGAATCATTTTATTTTTCAGAATACCTTACCCGCAAGCAAACTTT
CAAGCAAACCTTACAATTTGCAAAATTTTCATCGAATTCTCCGCAGGACATATTATAAAAGT
TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCCTTGTTCATTTGTTTTCCCAAT
TCAAACTCTTTCACGGAGCAGTTTAATTATCTTACTGTGCAAGAAGTCAAACTAGACT
ATATATTATTGAGAAGAAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA
CTGTTGTTGAACAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTGAGAA
CCGCTTTGGTTACGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA
GAGGTGAAGCTTTATTGGTTGTTTGGTCAAGTCTGTTACTGAAGCTAACATTATCAAGT
TGGTTGAAGGTTTGGCTAACGACCCAGAAAAACAAGGTTCCATTGATCAAGGTTGCTGATG
CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA
AGGTTGTCGGTGCCCTCCGTTGTTGTTGTCAAGAACTGGGGTGCTGAACTGATGAATTGT

CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVEEVVEVQEETVVEQTAEVTTIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV
VLVSSVTEANIIKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV
VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTCGATGTGCGACCAGATTGGGAATCTTACGA
CTATGCAAAGTTGGATCCAATAACGACGACGACAAAGAATTCATCAATAACATGTGGGC
CTGGGATAAGCCAGTTTCCGTCAATGGCGAACCAAGGAAATTGTTGACGGTAAGGTCTT
AAAATAATCTCTTCGTACTATCCTTCATGTGCGCTTTTATTATAAAGTATGCTAGGTAGT
TTTATCTATATCTTATTTATGACGCAATATAGGGTAACAGAGTTTTTCTGCTCTGAAACT
TCCGCAGAAAAAAATCAAGTTTTCTTTTCGTATCTTGGATTATTGTTATATAATAGAT
GCATGTATTATATGTATAGCAGTGATTGCTTATTTTCTTGATTCTGAGGAATCGAAGAA
GTAACCTAGCGTTTTCTTCCGTTGAGCAGAGCAGTATAATAATCCTTCAAATTCCTTAGGT
TACGGGGTTTTCTGTTGCGATGACCGAAGAACTATTACTATAGATTCTATTTCAAATG
GGATACTGAATAACCTGTTAACCACATTGATCCAGGACATTGTAGCTCGGGAAACCACTC
AACAAACAATTGCTGAAGACAAGATATCCGATCTTCGCAGTTATTATTTCGACCCGAACG
GATCTCTCGATATTAATGGACTACAGAAGCAACAAGAGTCCTCTCAGTATATTCACTGTG
AGAATTGTGGCAGGGATGTGTCCGCAAACAGACTAGCAGCTCATTTACAGAGATGTTTGA
GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDSISNGILNNLLTTLIQDIVARETTQOQLLKTRYPDLSYYFDPNGSLDING
LQKQQESSQYIHCENCGRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:
901-1605 (SEQ ID NO 271)

GTAAGCAGAAGCCGGAAGAAGACAAGAGGTTTCATTTCAGAGAAAACATCCGTACATTCGAG
TTCTCATTGAACCCATACATTTCAACTATTTTTACATAGTTCGTTTTTCATGTGTAAAT
TGTTCATCGACGCGCCGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCCT
GGGCGCGTCATTCTGTAGGCAGGAAGCCATGGACACTCTGCCCGTTCCCCTTGGAAAG
ATTGGCGTAATTCACGCTCCTCTATCGATTCTAGCGGGAAAGTTATCTCTCCTGGTAAG
CGTTGGAGGAATGCCGCTACCTAGGTAAGTCTACTGGGTGGGAATTCCAGTACCGACGTC
TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTTCATATACAGTGTTACCAAGGATAA
AGTGGTTAATGCTTATTCGTCATTGAATTTTTATATTTGCTTAAGAGAAGTGACAAAAGA
GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGCAACA
GAGAAGTTTATATGTGGAAGAAATGGCATGAAAGTTTGAAGTGAGAAAGAACTAAACAGA
ACCAGAGCTCGTAAAGATTTTAGAAATTTTATGGAAGAAGCAGGAAGACTACCATAT
ACTAATTGATGCGTTTTGTGGCGTTATTTTTAAACAACAGAGCGGGTTTACATATATGT
TACTACAAACCGTGAAATTGAAGCAGTTCATATACCTGGAGTATAGTCAATAAAAAGACAA
GCTTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCCTATTCAAACA
TTAATTTTGCAATAGTATACTAACAATTTTCTTAATAACCTGTTGAAAATTTAAATAG
TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAAGACCTTCGAAATTGATGATGAACAC
CGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTCGATGGTGAAGCCGTTGGT
GACGAATTCAGGGTTACGTCTTCAAGATCTCTGGTGGTAACGACAAACAAGGTTTCCCA
ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAAGCTTTCT
TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCCGTCAGAGGTGCCATTGTT
GGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAGGGTGAGCAAGAATTGGAA
GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA
AAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTTCGTGATTTTCGTATCAGAAGAGAAAGTC
ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA
AGATTGCAAGAAAGAGACACCAAGAGCTTTGAAGGTCAGAAACGCTCAAGCTCAAAGA
GAAGCTGTGCGCAATACGCTCAATTGTTGGCTAAGAGATTGTCTGAAAGAAAGGCTGAG
AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEV DGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD LAVLALVIVKKGEQE

LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQKRHRQALKVRNAQAQREAAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)

GTCTCAGTGTGCAATCATCATGGCACGGGCATTAATTAAGGTTAAGGAACCACTTCTCT
ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA
GTCATTGCCATGGATTATTCATCTCTTTTCGCTGTTCTCTTTCTTTTCAAGTTTGTCTATC
ATCATGCCCTTCACTTTTGCTTTTCCATCTTTTCTTTTGTCTGCAAAAATAAAGGGAAGAGGG
GTAAAAACGCAAGGAAGAACAAGAAGAAGAGGGTAGTGCAAGAAAAAGAAAAAGAAGAAAA
AAAAAAAAAAGTAATCTTGATACCGTGAGCAAATAAGCTAACGGAAGCGTAAGAAAGAA
GAGCGTGTTTTGGGAAATAACACCACAGCATAAAGCTAAATTCAGTTTATATAATCTAT
AGTAGTCCTATAGAAATTGCGAATAACGGAACAATAGTCCACCAAAGCAAGCATAGGGA
GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTCGATGTGCCCCGTAGATTGGT
TGTATAAAGGTAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCCTTCTACGTCGC
CAGCCTCCTCTTCATCTACGTCCTCTTCGAAAAACGGAGACAATAGCACGAGTGGTAACA
GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCATCTGTATCCAATGCAGCACTTTGTA
ATACTGAGAAACCAGATTTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA
ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA
ATCCGGCTACCGTAGACGCCATAGACCTTATAGATAATGATGACAAACGGCTCAAGTACTC
AATTTGTAAGGAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA
GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTTGGCAAGGGAAGCACC
CGCCAAATTTCTTACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGAGAAAA
AGACTAAAAGGTCGATTTTGGATCTTTGTTTAGCAAACGGTCTACCTCTTCTTCAGCTT
CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG
GCATTAAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATACCAATGAGAG
GAGTGGCACCACAGCTAGCAAGCCACAGACACCTATACTCCCCTCCCCTGCATTGACAG
TAAAAGACCTATCTACAGTTTCATTGAAAAGGCTCTCGTTTGCCGTCGATAAAATTCGAAT
CCGATCCTCCCCAACAACTTCTTCAAGAACCCCAAAAAAGGGAACATCCTTATCCCTG
ATGACATGATAAGCGAGGTTCCCTCTATTTCCGTTGGGTATTTCCAGTAGCAACCAATCCG
CCAAGTCAACCAATTCCAACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA
TACTCGCCCTGGAAAATCAAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG
CTCATTTTGCTGCTAATAGAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG
CAGGCGGTAAGCTTACTGAAAAGTCATCAGAAAGGCACCATTAAGCAAGCAAGAGAGAGG
TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACC
TCTCAAAAGCCGGCATTGATAAGCCCATTCATATGCATGAGCACTATTTCAAGGAACCTG
ATGACATGATAAGCGAGGTTCCCTCTATTTGAAAATAACGAAGTTACGCTGGATGTTA
TTTACACAAGATGCTGCCATTTAAGGGAAAATTTTACCCATTCCGCTCTACCTAAGACAAG
TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTTTTTTGAACCCTAAGCCTACCTTGA
TCGATATTCTTTCTTTTGTGATTTTCATCACCATTGCTCCCATTACACGATTGTTTTCTG
ACAATGTAGCTTTAAACCAGGATATGTTTCAAGATAATTTATTTCTGCTTTGGTAAACTCCA
CAGTTTGGACAAATTGAGTTTAAGAAATGTACGAATCGACCAAGATGGATGGAAATTAC
TATGTAAGTTTCTTTTGTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA
TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAATTTGTTTACTG
ACGCTTGTCTCAGAGATCTCAGAAACCTATAGAAAGATTGTTATTCAATGGTATTCAAT
TTAGCAAAATTCCTTACTCATGCTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAAA
ACTTTCCAGAATCGGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC
AGGATTGCTGAAATTTATCTTCAATTGGATGTCTCAATATAACGTCCAGGGTGTGGATC
TAGCGTTAATGATCTGTCCACTATGATTAAGCCAATGGTTGGTAAACTATCTGCTCTAT
CATATGATAACTTAAGATATTTCAATTTGAACAGCACTAATATTTGACTTCTTATGATT
TAGCTTTGCTCTTGAAATATCTTTCTAAGTTAGCTTAAGTTGATTTTGGATTTGAGTA
ATTTGTGCGCAATGCTTTCTGACATTTTACCCCTACATGTACAAGTATTTACCAAGATTTT
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAAGGAACTAGCTGTCTG
TTTGTAATATTTTGAATTAAGTGCAATCGCTCTCGCATGTGTCAATGACTAATCAAAACG
TTGAAAACCTTCTATCTAATGAACGGCACAGATTCTCCCGTTCAACAACTAACACAGACG
GCGACTTGGATAGTTTCGAGCACATTGGACGTTAAGGGCCAATTTGCTAAAAATAGTTTTT
CATCCACACTTTTACGCATTTGCTAGAGACTCTCCAACTTGATTGGTTTAGATTTTGACT
ATGATTTGATATCAGAAGAGATTCAATCAAGAATAGCACTGTGCTTGATGAGAAATATGA
AACGGACCATGGATTTCGACTTTCCAGTTAGATGAATTTGGATTTCGAAGATGATTGCTAT
TCGATGGCTCTTTAGTAACTATGACCGCTGAAAGTGTTTTAGAAAACTGAACTTGTATA
GCGATAAGAGTACAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAAATATA

TTGAAAAGTTCCATATCTTGCACCATAATGTTTCAGCATACAATAGATACTATGTTTCGAAA
AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAAACCTTGTAAAGATTACTCCTTT
TGGAACAAAACCTTATGCAATATACTAGAATTGTTTTTCGCATAATCCGAATCTGAATGATG
TCCTTGGATCCAGCAGGGATGATTTCGAAGGAAAGTGTGACTCCAGCGAAGATTCAAAT
TACCAGCATTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAATACAACCTG
AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAAACCTATTG
ACGTTTTTCACAGGCAAACCATTTGGTGTTCAGCATACATCATCTAGTACTTCTGTAGGTT
GTAAAAAGCAGGAAGAAGAAGAAGGTGAACATACATAAATGGGGTTTCTTCGTTTCAGCAGC
AGAGGTCTTTATACCTGAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA
CGCCTATCAACACAGAAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA
ACAATGAAACTGCTACCACTAGTTTATTTAGCCCAGCTAATCCTAAGATTTTACCAAAAA
TTCCATCCGGTGTCTGTCTTAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG
ATGATTTGATTTCAGAACGTTAACTCCAACAACATAGAATTGGAGAACATTTATGGTGAAT
CCATTCAGAATAGCGCTTCGACATTTACACCAGGCGTGGATTCTGATGTATCTGCGCCCA
ATACCGATAAAGGATCCGTAGAAACATTGCCTGCAGTCTCAACTGACGACCCAAATTGTG
AAGTCAAAGTCACTGCTACCTATGACAACTATTAAATAATTTGTCGATGGAGAGGTCAA
TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDVPVDWLKYGKSRKTNTPSRPSTSPASSSTSSSKNGDNSTSGNRSSNDKP
RARSSSVSNAALCNTEKPD LKRNDGNTSASDTDNIPLLTPINSGNRSDSADIDNPATVDA
IDLIDNDDNGSSSTQFVRKKRSTSI SNAVVS SKPRLASSAINATASSSVGKGKHPPISSPS
NATLKRSNSTSGEKT KRSIFGSLFSKRSTSSSASTAKKPLPVVNTSTENESGGIKAVAT
PDPRVKEISSPMRGVAPTAS KPTPI LPSPALAVKDLSTVSLKRVSFVDFKFESDPPQQL
PSRTPKKGNILIPDDMISEVPSISVGISSSNQSAKSTNSNIKGPLYTKKSKEYILALENQ
KLALREAAKHQGEAHFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPNVE
ADRELENNKLAENLSKAGIDKPIHMHYHFKEPDQDKYQDGH SIENNEVTLDVIYTRCCH
LREILPI PSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITI APIHTIVFDNVALNQ
DMFRIIISALVNSTVLDKLSLRNVRIDQDGWKLCKFLLLNKSLNKLDISQTKIKSDLAE
SLYRHNMDWNLF TDVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI
RLGLAGATTSNISQDCLKFI FNWMSQYINVQGVDLAFNDLSTMIKPMVGKLSALSYDNLRY
FILNSTNISTSYDLALLLKYLSKLPNLIFLDLSNLSCFPDILPYMYKYLPRFPNLKRIH
LDSNNLT LKELAVVCNLIKCKSLSHVSMTNQNVENFYLMNGTDSPVQQTNTDGDLDSSS
TLDVKGNF AKNSFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST
FQLDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKD TTKRYLLKKYIEKFHIL
HHNVQHTIDTMFEKRKSGELPLQEKENLVRLLLLEQNLCNILELFSHNP NLNDVLGSSRD
DSKESVDSS EDSKLPALKHVESGYHVPEEKIQPENDVITARPHLMATDSGKTIDVFTGKP
LVFKHTSSSTSVGCKKQEEEEGELHKWGFFVQQQRS LYPENESTRQTPFASGDTPI NTET
AGKSTSSPSVSTSNNETATTS LFS PANPKILPKIPSGAVLRS AIMKAKGIDSIDDLIQNV
NSNNIELENIYGESIQNSASTFTPGVSDVSAPNTDKGSVETLPAVSTDDPNCEVKVTAT
YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAAGCGATTTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC
TCAAACAGCATTATATCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCCTGTC
GGTATGAAAATTTAAAAATATATAATAACATAAGTTTGCATTCATTAATATTAATATAAA
TCAACGTATCAACCATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG
CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTTCGCT
CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTTAAATAACTTAGA
TGTTTTCTTTAACTTATTCCGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG
CTGTGCAACATTATAAAGGTGCTTTTAAACTACTAATCGTATATTTCAGCAGGTCAGAAC
GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCCGCCTTTATCAA
GGAACAATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAGATTTTCAGTCTTCCTTTA
CGTTCTTAAGTAACCAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAGG
CGAGTAAAAAGGCAGCGTACCATCGTCAACCCCGGAACACGAACATACTGCACCCTTA
TAAAGCAAAACAAGACAATCACAAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTAA
AAAAGAAAAGAAGCGATTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC
AGAGTGACATGACCACAAATGTACTCTATTTCTGGATATAGACCCTTATTCATCAATCCCA
ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG
AAGATTTAAATGAACCTCTATCACCATGGATTTCTCTGCCACTGGACTTGAATTTCTTTT

CAGAGTGGGAGAATATACCTAGTGAAC TACTGAAAAATTTGAAGCCTTTTCATCCACCTA
AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG
TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAAATGGATGAATTTCAAAGAGAAGAG
GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAACTTGAGGGAT
GA

YPL159C, 253 aa (SEQ ID NO 276)

MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKS KRKKGSKKAAY
HRQPPEHEHTAPLIKQNK TITKKEHSDVRGSHLKKKRSDFSWLPRVPSTSHLKQSDMTTN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKNLKPFPHPKEKSMNTNELIHVSAKRNTLVDNKTSETLQRKMDEF SKRRGKGRKKS
VVTLLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2:
569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC
TGCGGTTCTTCCATCCCCATCTCTTCCACATATACCGGGGGTTCTGATGGCATTCCCTATA
GCTTGCTCAAAGTCCTGCGAGTTTAGCTCATCTTG TGAGTTATTTGCTGGTTCTTCAACA
TTCGGAAGAGTAGTG TAGCCCTAGTATTACCATATGCCTTTGTATACTCATATGCGAAC
TTGTCTAATACAATGTATACCAAAAAATAACAGCTTGAAAAAAATCTCAGGGTCTTTTCAT
TGAATAATCTCATCTGCTATTTTAAGTTTTTCGTTTGCAACCCGAGACTGTGCGAGCTAG
AAAATTTTCATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAAACTTAT
GCAAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC
AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA
GATCTCTTTTGTGTTGATACTAACCAGTAAAGTTGAGAGTTATAACAATGAAATAGGA
TGCTGTGCGACTTTTTTTATCCACAGTTAGGTGAGTCGAATTCATATATATCATTTAT
CGCAGAAACTAATCGATTTGGGCCATTCTGTGCTATTATAACTCAGCTTACAAAGATC
GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA
TTTTTCAGAGAAACCACTTTCCCACTGTTTTTTCAACATTTCCAATAATAAGGAATATTC
TTCTCAGAGAGCAGATCCAAATTGTTTCATTCTCATGGTAGCGCTTCCACGTTTCGCTCACG
AGGGAATTCTTCATGCTAATACTATGGGATTGAGAACTGTGTTACGGACCATTCACTCT
ACGGTTTTTAATAACTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA
ACATAGAAGCGGTTATATGTGTTTCTAATACATGCAAGAAAAATATGATTGTTAGAACAG
AATTAAGTCCTGATATAATCTCAGTAATTTCCCAACGCAGTGGTGAGCGAAGATTTCAAAC
CAAGGGATCCTACTGGTGGCACCAAGAGAAAAACAAGTAGGGATAAGATAGTGATCGTGG
TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTTACTTACTCGCATAATTCCGAAAG
TTTGTTTCCTCACATGAAGATGTCGAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG
ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAAACGTGTGCAACTCTTAGGCTCTG
TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT
TAACAGAAGCATTTGGTACAATTTCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTGTAA
CGACACAAGTCGGAGGAATTTCCGAAGTGTTTACCAAATGAGATGACTGTTTATGCAGAAC
AGACATCCGTTTCTGACCTTGTTCAAGCAACAAATAAAGCTATCAATATCATAAGAAAGTA
AAGCTTTGGACACTTCCTCTTTTCATGATAGCGTGTCTAAAATGTACGACTGGATGGACG
TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA
AAGATTGGATGAAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC
TTTATCTGTTATGTGGAATTGTAGAGTACATGCTTTTTTTTCTCTTAGAGTGGCTATACC
CCAGGGATGAAATCGATCTAGCTCCAAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA
AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)

MSSSHKVESYNNENRMLC DFFYPQLGGVEFH IYHLSQKLIDLGH SVVIITHAYKDRVGVR
HLTNGLKVYHVPFFVIFRETTFPTVFSTFPIIRNILLREQIQIVHSHGSASTFAHEGILH
ANTMGLRTVFTDHSLYGFNNLTSIWVNKLLTFTLTNIDRVICVSN TCKENMIVRTELSPD
IISVIPNAVVS EDFKPRDPTGGTKRKQSRDKIVIVVIGR LFPNKGSDLLTRIIPKVCSSH
EDVEFIVAGDGPKEIDFQQMIESHRLQKRVQLLGSVPHEKVRDVL CQGD IYLHASL TEAF
GTILVEAASCNLLIVTTQVGGIPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWM DVAKRTVEIYTNISSTSSADDKDW MKMVANLYKRDGIWAKHLYLLC
GIVEYMLFFLLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTCGTGGAAA
ACCAGCATTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGTCTATCAA
TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA
ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT
GAGGCGAACAAACACATCTATACATATATATACATCTATATGGATATAAAAACGACTAAT
TCAACGTTGTTTTTATCAACCGAGCTTACTCTTGACGGGTAACCGCAAGGATAGCTAGT
TGCGGATGGTATAGCGATTTGGCTGGCAGCATGATTAAGGAATCCAAACATCTAATGGAC
TAGCACATTCTATCGATTTACGGGTCAGGTAAACATAGATATTGGGATATATCATATATC
CTTACTGAGTAACTATAATTATGGTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG
TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTCGA
CTAGGTCGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTGGCTAGAGTTTAAACACATG
ATGGCACCCCTGGATAATGATTATTTTAATAAGCACAAACGTTTCTCAGAAATGCAAGAGTT
CTGATGCAC'TTTTTCAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAACAAGAG
TAAAGTCCAATCAAGGAAAAAGATCAGCATCCTTTTCATAGTCCGGTGCATAATACGCTGC
TCAGTCCAAAGAACAGCAGTCATTCTAATACTGGAAGTCTGGTTCGGCCTGAAACCAC
GAAGAAAGTAAAAGTACCCAATCTGTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA
GTGAATCTACTACTGACGAGGAGGTGGAAATGTTTTTCGGAAGACAACATTGAAGATGGAA
AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAGAATGTGC
AGCAATTAATAATCAGAATGAATTACAATCCCCGGATTCAATAGATGAACAAGAAGATA
AATCAGGTACTGATGGAAAGGAAAAATCATAGAGCTGTATCCTTACCATTACCTCATTTAT
CTTCCAATAACTATTTTCGGAGAATCAAGCCATTCTATAGAACATCAGAAAGATGGAGAAA
CATCTCCAAGCTCAATTGAAACAAAACCTGAATGCAACAAGTGAATCAATGAAGAGGGGC
AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAAATTTGA
GGGCTCATTTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAAA
AAATCTTGTGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCATT
CAGATGAACAGCTTTGATCAGGAAGATCACATGATGCCCTAGGAGTAATTCATCAAGAA
AAAGCGACTCGAGCTTTATGTCTCTTAGGAGACAAAGTTCTAAACAACACAAATTTAA
ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG
AAGGGCATAGCTTACTGGAAAATTATGCGCTAATATGATTCTCTCCAGTCGACTGGAG
TTGAACGTAGATTTGAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG
ACTCGGGTGAGCATATGGCTTCAGGTGATACTTTTAATGAACTGGATGATGGCAAAATTC
GCAAGAGCAAGAAAAATGGTGGAAGATCTCAACTTGGCCAAAATATACCGAACTCTCAGT
CTACTTCCCCACCATTGCTAACATCGGTAGTAAAGATAATAATGTACCACAGCACAAC
TTTCGACCTCCATATCGAGTTTAAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC
ATGGTTCAAGAATGAATAATATTTTTCACAAAGAAAGGTAATCAGAATCTACTTCTGAGAT
CCAACGATCTCAACAAAATTTCTGCAGCCCCGGCTCTCCATTGTCCAACGAACATATTA
CATCTAGTACGAACCTCCGGTAGCGATGCAACAGACAATCCAACCTCAGGTGCCAAATTTA
ATAGCTTCGCCCAGTTCTTAAATCAGATGGGATTGATGCAGAATCAAGAACACAAAGAA
AATTATGGTTGCAGAGGGAGAATTCTATTATGGACTTAAGTTTCAAAAATGACGGTAGTG
ACTCTACTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATG
AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTGTTGAGATCAAC
CTATAATAACGGGAAATGCAATAATATCAGGAAAAAAGCCATAACGATGCTCAGTCAA
TCGCACATCTTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTACTAACT
ATGACAAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAAGATTAGGCAGTGT
TGTCCGGTATATGGAAAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA
AGAATAGGACAACGAGTACAAACCACAGCGTTGGCCACACTGCTTCACAGAATGCACGTA
ACTTGCTGAGGGGGCCGATGGGTTCCAGCACGACTTTGCACCACCAACGCGTCATTAAC
CTCTGCAGCCGACTACGAGGCGAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA
CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLSNASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND
YFNKHNVQKCKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFGLKPRRSKSTQSVLSLRDAQESKKSESTDEEVECFSEDNIEDGKVNNDKV
IAEHVMPPEKKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHSIEHQKDGGETSPSSIETKLNATSVINEEGQSKVTKEADIDDLSSHSONLRASLVKA
GDNISEAPYDKEKKILDVGNLTAAHKSNOQKPSHSDEQFDQEDHIDAPRSNSSRKSDSSFM
SLRRQSSKQHKLLNEEDLIKPD DISSAGTKDIEGHSLLNYAPNMILSQSTGVERRFEN
SSSIQNSLNEIHDGSEHMASGDTFNELDGKLRKSKNGGRSQLGQNI PINSQSTFPTIA
NIGSKDNVPQHNFSTSISSLTNNLRRAAPESFHGSRMNNIFHKKGNNQNLNLLRSLNLDNKN

SAAPASPLSNEHITSSTNSGSDANRQNSNGAKFNSFAQFLKSDGIDAESRTQRKLWLQRE
NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA
NNIRKKSNDQAQSIHSSSDTDHKDEDDLLFTNYDKKFDDLYPHLASAKIQAVLSGIWKS
ESYLFNKDVNPINKNRTTSTNHSVGHTASQNARNLLRGPMGSSTTLHHQRVINSLOPTTR
AVNRRMENVGVMHTQPQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:
668-1212 (SEQ ID NO 281)

TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTTCATT
TGTTCCCTTCCCTTATTTCTTTTCATAGTATTTATTTTTATTTATTTATTTATTTTTTTT
GGATTTTATTTTATTTCTTTTTTAATGCTAAGAAAGTAATCCGCATAATTAAACGTGTG
CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA
CTTCTACAAATTCGCGCTCAACATGGCCGTATTTGTACATTATATCGTTCTATCATATATC
GTATACGCCCGCATTACCCGACAACCTCCGTCTGCAACGCGTTGACCAGAAAACTCGAACA
AGAGATCGCATAAAAAACCAAAAGGAAACGAATTACTTGTCAAATAGTTATTGTAATGGA
TCCTCTAGAAAAGGCAAACAGTAGATTTATTTCCCTTCTTTTCTAGAAACATCATTATAACT
AACAAATATATAATTGGAATAATGGCTGGTTGGGATATTTTTGGTTGGTGTATGTTATCAC
CCTGTTTACGTTTTTTCGGATACTTAGTTTTATTTCAATGTGGTAAACATTGAATGTTTTCA
GCTTAAGATCTATTTTTTTTTTTCTAGAAGAAATTGCGTCCTTTACTAACTTTATTTTAC
TGTACAGTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACTACTTT
TTCTTGGGTTTGGATAATGCCGGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA
TTGGCAACCTTACAACCAACATGGCATCCAACCTCTGAAGAACTGGCTATTGGTAACATT
AAGTTTACAACTTTCGATTTGGGTGGTCATATCAAGCTCGTCGTTTATGGAAGGATTAT
TTCCCAGAAAGTTAATGGTATCGTCTTTTCTAGTCGATGCTGCTGACCCTGAAAGATTTGAT
GAAGCACGTGTCGAATTAGATGCTTTATTCAACATTGCCGAATTGAAGGACGTTCCTTTT
GTAATTTCTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT
GCTTTAGGATTTATTGAATACCCTGGCTCTCAAAGAATTGAAGGTCAAAGACCAGTTGAA
GTTTTCATGTGTTCCGTTGTTATGAGAAATGTTTATTTAGAGGCGTTCCAATGTTTATCT
CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)

MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE
ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA
ELKDVPFVILGNKIDAPNAVSEAEELRSALGLLNTTGSQRIEQRPVEVFMCSVVMRNGYL
EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)

TTCTTTTACAATTCACCTTGCAATTATTGAAGGAGTGCTATTCTTCGTTTTGCCACCCTTTT
GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCCCTGCGACAGCGCAACAT
CCAACCATCTAAAGGTATGGGTGTACTGACGATGCGATTATTTTATTAAAGTTCTGTCTT
TTTTGTATAAATGAAAAAAGAACGGTGAAATCCATAGAAATACAGAGAGCGACGCAAAACA
GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAAGCTTT
TTCACTTTGCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCCTCAGCTAT
GCGAAAGTTTCATTGTTTGATACATCTTGATAGTAACCGCAGGCTTCTTTCTTAGTTCAT
ATTTTATGTATTTCACCTAATATTATTTTTTTTTTTCAGTGGAAGGGAAGGTGAACCAAGA
ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAACCCCTATGCGTGATTTGAAGA
TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAATCTGGTGACAGATTGACCAGAGCCT
CCAAGGTTTTAGAGCAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACCGTTGGTAACTCCACAAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGATGCTGATGTTTGGACA
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKAQNPMDLKIIEKLVNLISVGESGDRLLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKCKGTGNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457)

TATATGACGGCAAGTGTCTCACTGTTGCATTACGCGATGTTTCTTTCTTTGTTCTTGTAAG
CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC
ACCGCTTTATTAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCCATTTATTTCTCA
AAGTGATGCGAATTTTACAGAGAACACATTAACCTGGGGGCCATAAACCGCGACGTGCTACCATT
TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT
ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTTACT
TTTCGATTTCAATTTGCGACTGCATGATGCTTTTCTTAGGTAGTTTTTGTATTAAATAGTA
TCATAAATTTCTTGTCTTTTACATAAGAATTAGGAAAGTACAGAACAAAGAGCAAATTTAATA
TATAATGTCCGGTGGTAAAGGTGGTAAAGCTGGTTTCAGCTGCTAAAGCTTCTCAATCTAGAT
CTGCTAAAGCTGGTTTAAACATTTCCAGTTGGTAGAGTGACAGAGATTGCTAAGAAAGAGGTAAC
TACGCCCAGAGAATTGGTTCTGGTGCCTCCAGTCTATCTAACTGCTGTCTTAGAATATTTGGC
TGCTGAAATTTTAGAATTGGCTGGTAATGCTGCTAGAGATAACAAAAAACAGAAATTTATTC
CAAGACATTTACAATTGGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAATGTT
ACCATCGCCCAAGGTGGTGTGTTGCCAAACATTCACCAAAACTTGTGCCAAAGAAGTCTGC
CAAGACTGCCAAAGCTTCTCAAGAACTGTAA

YBL003C, 132 aa (SEQ ID NO 458)

MSGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAA
EILELAGNAARDNKKTRIIIPRHLQLAIRNDDELNKLGNVTIAQGGVLPNIHQNLLPKKSAK
TAKASQEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459)

TGAACGGGTGCAAAATTTACTTTAACACCCAAAAAGTATATGCGTATATATATATATATTTATC
CTTGTTATTTTTGTAAATTGAGCTATGCAACATAAGATTCTGCGATGTAAGAACTACTTGC
TAATCAAGAGAACTTCAACAATTTTCCATCGCAGAGACGAAAAAACTGGAAAAAAATAAAAA
GAAAAAATTGAAAAAGAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT
TCTTGACATCATCAACACACCATCGCAGACCCACGTGGCCGCTTCGTGTGCCTTGAAAATAC
AGCCTTAAACGCAATCTCATTTCGCGTTCTGTGGAAATTGTCTCGGACTACACGCTGGGCGTG
CATCACCAGTGAAAATGCCGTACCGCCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA
GAAATAGACTTCTGGGTTTACACCCCGGAATAATACTAAAACCAAACTGGTAAATAGGGCT
ACAGATGAGCAGGAAAAACGTTGCCGAAAAAGTTTATTTATCCGAGAGAATAATTGATGAAG
AAGTAGCGGTATGCACAGTAGCGCGGAAGTATTAGCAATTTTACTCTGTTGTGACAGA
GTGTTTCATCATTTTTTTTACGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA
GAGACCGTACCACACGTTTAGAGCAGCCAGGTTGCGAAACTCTTCTAAGATGGTTTCCAGCA
ATTGTGTACTATCAGAATGTGGACAGTTTAAAAGGTTGACTGCGAATTTGTCCCAAACCGTA
TCACCGTCGCATTTTTTTGAATTTGATCAAAGCACCCTCCTAATAGCACAGCGATGCTGTGA
GTGTGCCAGTGGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460)

MSRKTLPKQVYLSERIIDEVAVCTVAAEVLAIFTLVCTRVFIIFFTARICHGIWPSSPSER
PYHTFRAARLRNSSKMVSSNCVLSECGQFKRLTANLSQTVSPSHFLNLIKAPLLIAQRCEC
ASNGC

YDR529C, 884 bp, CDS: 501-884 (SEQ ID NO 461)

GAGTCTCCGGAGTTGACCAAGTCATACAATGTGCTACTGACCAAGAAATGGATCTGTGTAGT
TCCAAGATCGCATGCCAAGAGTGGACCGCCATTGATGTTAAACATTAACCTCCACGGGGTACT
GTGGTATGATCCTCGTTAAAGACAGAGAAAACTAGAGAACCTCACTGAAGATCCTCATCTT
GTGGACAAGTCGTTACTGCAATGCGGTTTCCCCAACACAGCAGGCCAAAAACCAACAGAGTA
TCACTATTAAGGTCTATTAGCCATATGTACATTGTCTATAGATGTGTAACCTGCGCTGTGATC
TTGTTTGTGACCAATCAGGAGCGACGCGCTTTTTATCGGGTCACCCGGCGGGGGCCTGACA
ATTTACTTTTCATAGAGCAGTAATAAAAAGGGAAGAGATGTAAAAGCTTGGAAAAATAGCAGTA
AAGGTTGTTGTTGGACAATTTATCAGAATATTAGTAACCTGTAATTAAACGTTCCAGAAAGAA
CAAAATGCCACAGTCTTTTACGTCTATTGCGAGAATTGGTGAATATATTTGAAGTCACCCG
TCCTCTCCAAGTTATGTGTTCCAGTTGCCAATCAGTTTCATTAACTCGCAGGTTCAAGAAG
TTAGGGCTCAAATTTGACGACTTAATTGCAGAGGAAAAATCCCATCATGCAGACCGCTTTAAG
AAGACTCCCTGAAGATGAATCTTATGCCAGAGCATATAGAATAATCAGGGCTCATCAAACCG
AGTTGACTCATCATTTTACTGCCAAGAAACGAATGGATCAAAGCCCAAGAGGATGTTCTTTAC

CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGAAGGACGAGTTAGACAACAT
AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462)

MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRR
LPEDESARAYRIIRAHQTELTHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIE
VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTTT
TTTAATTGTGAAGGAACAATTCAAGTTAGAAGTCTTTTGATAGGAAACATTATTTCTGTGT
AGCCTAATGTTTTAATGCCAATTTTTTCTAAAATGCAGCAACATACATATGTTGAGTCGTA
TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACATTTTAAAC
ATCCGTACAACGAGAACCATACATTACTTTTTTAAATATTCTTTTGTFTTCACCGCCTTC
TTTTTATTTTTATCCGAAGATCTTTTGGAAACCGCTCTGCGAATAGCGAAGCTAGGATACCA
AATTGAAACTTGGACATAACTCATCTATAAGAAGTATACTGTTAAGAGAGGCATTCATTTTC
GTGTATTATAACGTTTAGCATCAGTTACCCCTTGAAAGCCCAACATATACAAAAATACGCGTC
CAAGATGTCTACTAAAGCCCCAAAACCCCTATGCGTGATTTGAAGATCGAGAAATTGGTCTTGA
ACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCTCCAAGGTTTTAGAACAATTA
TCTGGTCAAACCTCCAGTTCAATCCAAGCCAGATACACTGTCAGAACTTTCGGTATCAGAAAG
AAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTCCAAAGGCTGAAGAAATTTTGAAA
GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAACTTCTCTGCTACCGGTAACCTTC
GGTTTCGGTATTGACGAACACATTGACTTGGGTATCAAGTATGACCCATCCATCGGTATTTT
CGGTATGGATTTCTATGTCGTCATGAACAGACCAGGTGCTAGAGTCACTAGAAAGAAAGAGAT
GTAAGGGTACTGTTGGTAACTCCCACAAGACAATAAGGAAGACACCGTCTCTTGGTTCAAG
CAAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRN
EKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSIGIFG
MDFYVVMNRPGARVTRRKCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465)

GCAACATTACCACCTTGTACGGAGCGTCAGAAAGAAGCACCTCATCATTATTATGAGAACA
GTACGATAACTTCTGTCTGAGATACGCTTCGTTGTTATAATACAAGTGAAACCGCCACGGAT
AATTAGCAGCAATTGAACACAAGGATATCATTTGTGTGACCTTTGTTCTCTCATAGTTGC
TGTGAACCCCTTTAGTAATTAATGTTTTATTTTATGAGACTAGTCAAAACATTCAATAACA
GTTTTTCTATATGAGAAAAAATGAAAAAGCAACAGTACGATTATT
ACACTGACTATGCTGCAGTTTCCGCAATAGCAAAATTGTGTACATTACACGAAAGAAAGAA
AGAAGCCTATTTCTTATAAGAGCAAACGTGTGATAAGTTTATAGCAAGAAATAAAAGGGTAA
AAAGTCATTGATAATAAACCCTGCTGTGACTATATATAATAAGAATCGAAGTTAAAGTTAA
AGCAATGGTGTTCGGTCAGCTGTATGCCCTTTTCATCTTCACGTTATCATGTTGTATTTCCA
AACTGTGCAAGCAGATTATCCAAGGAAAGCTCTTCCTTTATTTTCGTTTCGACAAAGAGAGT
AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC
TATCGCTGTTTTTGAATTTGACAATTTCTCATTTATTGGACAACCTTGATGATTGACGAAGAAT
ACCATTTCTTCAATAGATTCTTTGCCAATGATGTGAGTTTAACTGTTTCATGACGATTTCGCT
TTGAACATCTCTCAATCATTATCTCCATTATGGAACAATTTACTGTGGATGAATTACCTGA
AAGTGCCCTCTGACTTACTATATGAATACTCTTAGATGATAAAAGCATCGTTTTGTTCAAGT
TTACCTCGGATGCCTACGATTTGAAAAAATTAGATGAATTTATTGATTCTTGCTTATCGTTT
TTGGAAGATAAATCTGGCGACAATTTGACTGTGGTTATTAACCTCTCTTGGTTGGGCTTTTGA
AGATGAAGATGGTGACGATGAATATGCAACAGAAGAGACTTTGAGCCATCATGATAACAACA
AGGGTAAAGAAGGCGACGATGATATTTTAAAGCTCCATCTGGACTGAAGGACTACTAATGTGT
TTAATAGTTTCTGCGTTGCTATTGTTCAATTTGATTGTTGCACTTTCTTGGATATCTAATTT
GGATATCACATATGGTGCGTTGGAAAAATCAACAAACCAATAAAAAAACAATTA

YGR106C, 265 aa (SEQ ID NO 466)

MVFGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDTISTISSTADVISSVDSAI
AVFEFDNFSLLDNLMIDEYPPFNRFANDVSLTVHDDSPNLISQSLSPIMEQFTVDELPES
ASDLLYEYSLDDKSIVLFKFTSDAYDLKKLDEFIDSLSFLEDKSGDNLTVVINSLGWAFED

EDGDDEYATEETLSHHDNNKGKEGDDDDILSSIWTEGLLMCLIVSALLLFILIVALSWISNLD
ITYGALEKSTNPIKNN

YGR182C, 854 bp, CDS: 501-854 (SEQ ID NO 467)

CCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAACGACTTAGCGAAGCT
TATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCATTACAGGTTACTAAC
AATGCATAAATTATGAGTAGTCTTTTTCATCACTATATAAAACCTTTTCAAACGAAACGCT
GTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTCCTCAAACCTGTATTTGATACTGCTAT
TACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGTCAAGGCTCGAATAG
CTGCAGGCGATGGAGACGACGATGATGAGTAAACGCTGATTATGTCACACATATACGTGCAA
ACGCTCTCTCTCTCAAGCTATATAAGTGGCACTCGTCTTATTATATTTTTTTTATTT
TGGCTGGTTGTTTCATGTTCAACCCCAACCTCATAAAGGCACTCAACTTCATATTTTGACACAA
ATCTATGTCTCGCCAAAGCGCATTCAAAATTCAGAATGGAAATAGACACGAACGAGCCTGTC
TGTCAGATGTTTCAAAAATCCTTATTATAATTTTATATTCTACTAAAGGAAAAAGAGAATTA
GGAAAAAGAATAACTCATTTTATGTATATACATATATTTTGTACATATCTATACCAAGCAAG
TATAGTGCAATACTGTTCTTCGACGTATTTAAACGTAATAGCATTTTCTTGGTATCCTTTGA
ATCTTATATACAAGTACGAGTACATACTGCGCAGTAAATTGATCCTGATGGTGTGTTTAGAT
TTCGCCAGAAGCGGAGGCGTTCTGGATTCTGGAGATGTAAGCCTTTGA

YGR182C, 117 aa (SEQ ID NO 468)

MSRQSAFKFQNGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI
VQYCSSTLLNVIAFSWYPLNLIYKYEYILRSKLILMVCLDFARSGGVLDSDVSL

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-
914 (SEQ ID NO 469)

AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATAATGATGACTCTGATGAGC
GAGAGATTTGGTAGATTCAAGCCCTCTACTATGTTTTATAGTTGACATATTTGTATATAAAA
ACTTATACATTATTAACATTTGCGCGTCGATTGACTTTTATTTATTATTAACAAAGAAGTA
ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCCTTATCTAGCGAAGGC
AACTTTTGAACCTCCCAAGTTGTTAATATGTATCATTATACACGACCCAATCAAACGCGGGGA
AGTCAATGCCGAAAGAATTCTAGGACCTAAAAGCTGCTCAATCCTTGGGCTTTCCCTAATG
ACATCCCCTCTCAAACCTTTAGCTTAGCAGTTGTAATTTAATGTCCTGTACGGATAGTCAATA
ATCGTTGAAGTTGATTTTCATATCCTTCGCAATTTGTAAGCAACAATAGCAATACGGC
TAAAAATGGTATGTTGGTGTGTGTGTGCTGCTTCACATTTACAGCTAAAAAATGTTATCCGT
GGAATCTTCCTTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAAC
GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA
TTCAGGTTACTAACAATGCATAAATTATGAGTAGTCTTTTTCATCACTATATAAAACCTTTT
TCAAACGAAACGCTGTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAACTGTA
TTTGATACTGCTATTACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT
CAAGGCTCGAATAGCTGCAGGCGATGGAGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470)

MSFSSLYKTFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD
DDDE

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 471)

GGGCTTTTCCAGTGCCGCGGCCTCGAGATCCAGGCACCAGGAAGTACGGCAGCTGTGTATTC
TAACACATTGAAGGGCCTAGGCCCCGTGACGTGGGGTCTAGTTCCACTTTTTCATTACCTTT
TCTCGGTCTTTTCTTGCTCCACAGGCCGTTAATGGCCTGAAACAGTTTTGTGACTTTGGAC
TTATGATAACGATGTTTGTCCGGGTGCCACCGGATTCTATCGCGGCGAATCAAGTCTAGTCT
GTTTGCATCCATCAAGGCACTGCTCATTGTGTAAAATTGTTCTACGCTTTTGTCAATCA
TATCTAAACTCACAGCCGCTAGGGTAGGTGTGCCTGGCAGTGGTAAGGTAGCCGGCTCGTCT
TTGGTCATGCGCCAATACTGTGCAACGGCCCGCGGTAGCGTTCTTCCGCTTCAACCTTAGA
GCTGATACCTTTTGCCTGGTCAAAGGCGAAAACGCTACCTCGCTTTCAGTCTGCTTTTCGC
TTTTCATGTTCTGTTTCAAGCGGTCTCTTTTCGCTCTCGGTTGTAACACACTGTAGCCTGCT
ATGCTTTTACCCTACTCGAAAAGCGTAGCCTCATGACTAGTTGTACCAACGCCCTTTCTTTT
CTTTTTTTTCTCTTGACACTTCGGCGTATTCATCGCCACTGGTACAAGCCGTATGGTGCCTT
TTTGCTCATTTTCTGTTTGTGACGTTGCGATGGTTTCGCGGACCAATCGCATGGGTGGTGG
ATGTTGTCTTTGCTAGTTGCAACGTAGTCTTCTCTCTCCTGCGCTTTCTGACGAAAATTGG
CCTTACGTATCTTTTTTTCGGCGTCTGTGTCGTCATCGCTGTTTCATATAATCGTCTGCTCACTCA

TATCGGCGCTTTTACTGCATGCTGTCTTTTGAAGAGAGTTTCATTGAAAAGTAGTGAAGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAAGCTTACATACGGAAAAGAGAAAAAAAAAA
AAGAAATTTTAA

YKR040C, 167 aa (SEQ ID NO 472)

MTSFQAVSFALGCNTLVACYAFTVLEKRSMTSCTNALSFLFFLLTLRRIHRHWYPYGAFL
LIFVLTLRWFRGPiAWVVVDVVFASCNVVFSPALSDENWPYVSFFGVVVVIAVHIIVVTHI
GAFTACLLKRVSLKSSEEKKKKKKKKKEKSLHTEREKKKKKF

YOL127W, 1343 bp, exon1: 501-513, intron1: 514-927, exon2:
928-1343 (SEQ ID NO 473)

TCTTATCTTGTATGCCGATATAGCAACCTTGTGGTACCAATCTAACGGTTTCCGTACTTT
GCAATGAAGAGATGAGGAGGCATGGGTCACCTTATTTAATATGTACGGGTGTTTACATGGAGT
TGCTTTCTTTTTTTGTCTCAGCAGTCATTGTGCGCCAAAAAAGAGAAAACCGTGAGCCGAA
GTCCACGCTCTGGAGTTAGGCTCTCCCATACGGAGAGAAGCATTTCTCAGCCTGGGAGCC
CCGTGGAACAGTCAGGCTAACTGGGCCCTTCTACCCACTGCTTGCTGTTTCTCAGTGGAC
GCACAAGGGGATTTTCTTCTACCTTCGGCTTGCCCTCACTGCGTTGGGGCTTCCCAATGCAA
CTTCGTTTCGTATGCATACAATCTTTTAGATATTATCTTTTAAAATTATTTTAAACAATTTT
AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA
TAAAAATGGCTCCATCTGGTATGTGAAC TGCAATATTAATAGCACGAGAAAAATTGAGAGGAAG
ATAGATGGGAACTAGTAGAGTTGATATTGATGAGATACGAAAACCACACGTAAATAAACTAT
CCGACGACAAGAATAGTGCATTAAGGACTTGATTAAGATATGGTGAGCAACGTAATTATCGG
GCTCAACAGTTTATTAGCAATCGTTTGTAGTAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT
TACTACCAACAGCCATTAAACAAATCCATTAGAGTGTTCGTTTCGTTTCTGCTCAGATTCAA
GAAAAATTATCCATCCTCATTATACTTTTTCTTCTATTTTCGTGCTCCACGTCGAGGTATCA
AGGAACATAGTTTACTAACATTAACGAATTCATCTCCTATGAATTTACTTTTTGTATAGCTA
AGGCTACTGCCGCTAAGAAAAGCTGTCGTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC
AGAACTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC
TTCCAAGGCTGTTCCACATTACAACAGATTGGACTCATACAAGGTCATTGAGCAACCAATCA
CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTCCAAGTTTCCATG
AAAGCTAACAATACCAAATCAAGAAGGCCGTCAAGGAATTATACGAAGTTGACGTATTGAA
GGTTAACACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT
ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474)

MAPSAKATAAKKAVVKGTTNGKKALKVRTSATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV
IEQPITSETAMKKVEDGNILVFQVSMKANKYQIKKAVKELYEVDVLKVNTLVRPNGTKKAYV
RLTADYDALDIANRIGYI

FIG. 2:

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

AGAGAACGTATTGAAGAGGAGAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA
TCAAATGCTTCTATGGCTTCTTTATTGTCAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT
GTGGCTGGCACAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAAACAATTCC
CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTGGAAATTGTACACTCAA
TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG
AATATTTCTCAACGGAAAAATCATATCAATTTTATGTAATTATTTGAATTTATTAGAATTGTTTGAT
AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGATAACTCAACAATCTATT
ATTCCTAATTCTCAACAGGTGTCTGGGCCAACCTACCCGCAACAACATCAACAGAATCAACTTCAA
CAACAGCAACAGCAACAACATCAACATCAACATCCTTCACATTCATCATCGATGATGAACCTTCAT
CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCTGAATTATTAAGATCCCAATCGCAATCAGCA
TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC
CAAAATCAACCACCACAACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG
CAATCTATTCAAAGCCAACCACATCTGCGAGACCTTATTCTCAATCATATAATATTTATCAACAA
CAACAGCAACAGCAGCAACAACAAGCTCAACAACAAGCTCAACAACAACAACAACAACAATACAA
TATCAACAGGGACCAACAGGTCAAGTTTCAACACTCACCTGATGTAATTCTTCTAGTGTCTGCATTA
CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCACAAGTAGTTTGTCT
CAACAGCAACAACAACAACAACAACAGCAACAGCCGCCACTAACTTCATCAATCCATGATTCT
CCAACACCACATCATCATTTACCACTTCAACAGCAGCCACCACAACCAAATCATTACCTATCCAAT
TACCATCAGGGGGTTGGATCTCAACCAAAAACCTCCATTGGC

YBL051C_homolog_1 409aa (SEQ ID NO 286)

RERIEEEKREKRGQLEEQHRSASNASMASLLSAASTTAATKNLSVAGTNPSHTTERMFLNLPFNNS
SFNAPPVEINFNDLEVLLEYTLQVLVYRDDITKSTFELAI SPANLNISQRKIIISILCNYLNLLLELFD
NGLIIIRRKPGYIAQCITQQSIIPNSQQVSGPTHPOQHQQNQLOQQQQQQQHQQHPSHSSMMNLH
QLGGTLAVPAHPELLRSQSQSALPLPRLRQQTSTPIQONQOVQHQNQPPQQQQQQHVQPOYNYYNQ
QSIQSQPHSARPYQSQSYNIYQQQQQQQQQQQAQQQAQQQQQQQLQYQQGHQSQVSTPTLNSSSAAAL
LRSSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPPQPNHYLSN
YHQVGSQPKTPL

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

ATAAACAAAAAGAAGCACGAACTGTGGGCAACAACAACAACAACAACAACAAAAAATTT
CTGGAAATCAAATTTGAATCCAACCAGCAGCGGCGGGCGGACAGAAAAATATATTAACAGAAT
ACTTTTTTGTATTCAACTCTCTAACTCTTTCTATTTTTTTTTTTTTCTATATACACTGTTAAATC
AATCAACAATAGCAGGATATCCATTCATATACAAATAGATAAACTGTTTAATTAATTAATTAAGT
ATTTGATTTGGGAAAAAACAATTTTATATTTGGAGAATTGAATTTCAATCATTTTAACAATTC
AAGCTTTAATTTCCACCTATCAAAATTCATTATTATTTTGTTTTTCATTATTTTTTTTTTCCCTTT
TTCTTTCTTTCTTTCTTTTGGAAACAAGTAATAGCCGATAAAATAAATAATTCACATAGCCCA
ATTCATATTACATTGACTTTTGACAAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC
CGAATCAAATGGGCACTGTAATGCAACGTCTGTCCTCTCTATCATCATTTATCGTCTAGCCTCGGGCT
ATTCCTTCTTCCAATTATGGTGGAAATCCTACACCCAATCCCAACAATTCCAATACCAATAACAATA
GTAGTGGCAATAGTAATAACAACACTCATGGCAATAACACTCCCAATTATCAACTCAAAGATTGA
CAAATAATAGGAATTTACAATCCTTGTGGATAAACCAACCATCTATTGCTCCTTCTAATGTTGTTT
CTTGGGTGGAAACAGCAACAACAACAACCCCTTGATCTGTTGGAAAAATAACTATAAACAGACTCCA
GTAATGATGCTTCTGCTACTAATAATAATAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA
ATGCCAATGCCAATATCCATGCCCAACCCATGTCAACACAAATGTTAATGCAACACAACAGCAA
CTAGTATTAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA
AAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA
CTAACAAATAGTAGTACAGGAAGTTCTAACATTGCAACATGCTTCCTTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATAGCACCACAACAATACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCATTTGCCATTAAAAAGGAACAATTGT
TAGATGTGATGACAAAATTAACCTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG

YBL066C_homolog_3254bp PathoSeq: 1..94/2146..3254, public:
95..2145; CDS: 501..3251 (SEQ ID NO 289)

ATAAAAAAAGAAATACAATTAAAAAAATTTTCCTTCTGTGAAAAGGCAATTTCCGGGTCTAGTAGTA
AACAAAGCTTAATAATTTCTCCCATTCAAATTTTACAACGGACGATGCAGAAAGTAGTTTTCAAATTT
CAGTTCTTTTCTTTTATATATATTTTCTTACTTTCTCTTCTTCTTCTTCTGACAGTATATTAATA
AATATTTCTTTTAACTTATTTTTCATCAAGAAGGTACTGAAGATATCAATTAACCTCTCAGTTAAA
TCCATATTACCAGTTGTGGAATAATCAGAAGAAAAAAGAGAGAAAAATCACGGGAATTAC
GTTCTCAACAGAAAATAACAATAATTTTTTTTTTATTTCATTCCAAGGTATAACAAGAACGTTAGGAA
TAATATAAAATTATCACCAAAGCTGCCATCAACGTGTGTCGACAACCAATCGACTCCTCCCTTAAC
TAGAACCATAGAACCCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAAAAGGTAAGGTGAGAA
TTTTGCCCTAAACCATCCCCTACACCAACCAACCCACAAACCCCATTGCCATTACTTCCAGTCTCAA
CTAAACCCTGTAAACTCAAAAAGAAAATCAGCAGCCAGTACACCTGGAAATGAATCAAAAGAAATCAA
GAAAATCAAATTCTACAGCTTCAACACCCAACAGTGCTACACCAACATCAGTCGGAACACCTCCAC
AGAAAACCTCCAAACCAACAGGTCATAGGCCAGTGACTTCATGTACTTTTTTGTCTGTCACATAAAA
TCAAATGTAATGCTTCAGATAATTATCCAACCCATGTGAAAAGATGTAAAAAAATGGGTTTGAAAT
GTGAAATTGACCCCGAATTTAGACCTCGCAAAAGGGTCACAAATCCAATCATTGAAACTGGATGTTG
ATGAATTGAAGGCCAAGATTGAATGTGACTAAAAATGAATCTTTGCTCACACAAGCTTTGAATC
AACACAATTTGAACCAACGCTTTCGCAACAGCAACAACCTGTCTGGATTGCAATCTCAACAACAACATC
CTCCAAATCCACAACGTGCATTTGTCATATACGTCTGCAAACTCATCACCACAAGTTGCATTTAGCA
ATGCATCGCCAATTCCTTCTGTGACAAGTATTCACAAAAATGCACCGTTGACTCACGAAAAATCCG
ACAAATCTCCATACGCTTTAAATACACCAGAAAACATTGAAGAATTACAACCAATCTCAGAATTTA
TTTTGGGTGACGTTTACTTTGCCATTAAACAGGGCCAAATGAGTTACACGACAAGTTTATGACCACAC
ATTTACCATTTTTTGCCAATAATAATATCTCGATTCTGCCACCGAATTTGATATCAATAAATCTCAATTCG
TTTTCTGGGCGGTGATTCTTACCGAAGCTTATCAGAACCAGAACTTATATATGTCGTTGG
CATCCTTAATTAAACAATTAGCAATTGAAACATGTTGGATTAAAAACACCAAGATCAACTCATGTTA
TCCAAGCCTTGATCATACTTTCAATATGGCCGTTACCTAATGAAAAAGTTTTGGATGATTGCTCTT
ATAGATTTGTTGGATTGGCAAAGAACTTGTCAATTACAATTAGGTCTACATCGTGGTGGAGAATTCA
TTCAAGAATTTAGTCGGAATCAAGTAAGTCTAGGACCTGATGCAGAAAGGTGGAGGACTCGTTTCAT
GGTTAGCAGTTTTCTTTTGTGGAACAGTTTTTGGTCATCATTTGTTGGGTTGGCCACTTCAATAAACA
CTACTGATTATTTATATAGAAATGCTCGTGTGTGATAAATCGTTGCGCTAAAAAATTTCCGTTGTTTG

TTTCGCTATCTATTTTCCAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG
GTTTATTGGAGCCTCTGAATCGTGGTTCACCTTAGTTTATTGGATAGAGAATTGGAAAGATTAA
GATTTAAACTTCAATTTGAAGAAGGGGGGCCAATTGAAGTATATTATTTGTATATTAAATTGATGA
TCTGCTGCTTTGCCTTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTCAGTTTGCAT
ATTTATCAGCAACAAGAATCGTGACAATCGTTTCTAAAATGGTGAATGACATTTTCATTGATTGAAT
TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTTTTCATGTTGTTCAAATTACATTTGTCAA
GATATTTGATTGACAAGTATGTGGATAGTGCTAGACAGCTGATTGTTACTGTGCATCGTTTATTTA
GAAACACGTTGAGTTCCTGGAAAGATTTGCAAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA
ATTTGAACATGGTGTGTATAATTATCCTGAAATATTTTTAAATGATCTGGAAAATGAGGATTCAA
GTATTATCACCAGAATGAGGTCACATTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC
ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAGAAAATCT
TGCCCTTGCCATTTTACAACCAATCCTAAGGATGATTTCAAGACAATTACCACGACATCACCTA
ATGGAAC TACTATTACTACATTAGTTCCAAC TGAAGTATGAATCAAGCAAAAAC TGAATCTT
TTGATTCCAGCAAACCACTTGAAATAAATGGTATTCCTTACCTATGCTTGAAGCTACTGGTTCAA
CAAGAGAAGTTTTAGATTCTTTACCTCGCAATCTTTACCATCACAAGCACCAACTCTTCAGCAGT
ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAACAACAACAACAAAAGCACCTGCAGC
AACTGCAGCAATAACCAACAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC
AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCTTCAGCAACCAC
CTTTTATTTTGGCAAAC TACCAGTACCAAACTTATTTGCCAAAGATTGATGAAATGAATATGT
CACCAGAAGTAAACAAGAAAAC TCTGTTGCTCCATTTGCATCTCAAATCACCACCTTTTGTGATC
AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTGGGTTGGTTTGTATGTTA
ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLLPQTKPVNSKRKSAASTPGNESKKSRSKSNSTASTPNSA
TPTSVGTPPQKTSKPTGHRPVTSC TFCRQHKIKCNASDNYPNPCRCKMGLKCEIDPEFRPRKGS
QIQSLKSDVDLAKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYTSA
NSSPQVAFSNASPIPSVTISIQQNAPLTHENS DNSPYALNTPENIEELQPISEFILGDVTLPLNRAN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQGLHRGGEFIQEF SRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLL ENARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDG LLEPSNRAGSLSLLDRELERLRFLKQFEEGGPIEVYLYIKLMICCF AFLPGTPIE
DQVKYVSFAYLSATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMLFKLHLSRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENESSII TRMRSHLTAS
LFYDLVWCVHEARRSVLDKGKRAQPNKKILPLFYNQITKDDFKTITTTSPNGTTITTLVPTDQ
AMNQAKSKSFDSKPLEINGIPLPMEATGSTREVLDSLPSQSLPSQAPT LQQYPMQDQQQQEPS
QQQQQKHSQQSQYQQQQQSNQQQPHLQHQRQFQQSPPPQFSMISSTPPLQQPPFILANSPLPQTY
LPKIDEMNMSPEVKQENSVAFFASQITNFDQQTSGWFNNDNQDDDFLGWFDVNMMEQEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:
450..533, exon 2: 534..908 (SEQ ID NO 291)

TTATTATTACTATGACACACACTTACTCTCTTCTATGTCTCCGCTTACATCACACATCATACGTTT
GAAAACACCCACCCCTTTTCTTATCTACAAAAAAAATAACAAACTCACTATAACTACTAAAC
CTTTTTTTTTTATTTATTTATTTTGTATTTTGTATATTAATCAAATATTATCATTCATCTATATA
TACATCCCATCGATTCTGACATAATAGTATGTATGATCATACAGAGGGAAAATCACCTTTT
TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTGTGTAG
ATAATTGCCACTCAATCTTTAATTGACCATCGACCACAAAAATAATATGGAAATAATACTAACAGA
ACTTAGAAACATCACTCATAATGAGATCACAATTCAAAGACGAGCATCTTTTGGTGTATTATACA
TGATTTTGTAGTCTCTGAACTCTTCTCCGATCATCATATACTAACATTTTCGTGGGTGTTATTCTT
TAATAGAAAAGAGACAAGCCGAGGCAGCCAGAATTGCTCAGAGGTTCAAGGATAGAGTACCAGTCA
TCTGTGAAAAGGTTGAGAATTCCGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG
ATTTGACTGTTGGTCAATTTGTTTACGTTATTAGAAAAAGAATCAAGTTACCAAGCGAAAAAGCCA
TTTTCATCTTTGTCAATGACATATTACCCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC
ACAAGGACGAAGATGGTTTCTTATACGTTTATACTCTGGAGAGAACTTTTGGCGAGAACTAG
CAATTGACATTTTCATCATTAGATTTCACTGATATCCCTGATTATGTTTAA

YBL078C_homolog 135aa (SEQ ID NO 292)

MRSQFKDEHPFEKRQAEAAARIAQRFKDRVPVICEKVENSDIPEIDKRKYLPVDLTVGQFVYVIRK
RIKLPSEKAIFIFVNDILPPTAALISTIEEHKDEDGFLYVLYSGENTFGEKLAIIDISSLDFSDIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

GTGGCACATCCCAGGAAGTAGAGCATGGACAGTTCGTATGGTATTGCTGTGCATACGATACAAAAA
AAACAGAAACGAGAAAAAATCGATCGTCAACCTTTATCAACTCATCTACAGCAGCAGCAAAGTT
CGTCCCTAAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT
ACTTTTCATTTTCCATTTGTTATGCTTACGACAACCTGAAACCATGCTACTTCATACGTTTGTATTGA
TGTTTGGCCTTATTGGTTGCCATGCGGATCTACGCTTATTTGCCTTCAAGTATCATGTTTGCATCT
CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT
GTCTACTTAGTTTTATAGTTTAAAAATTTGTTAATATAAACCCAAAGTTTCTAACAGGCTCTGTTT
GCTCGACTAAAAAGAATTTGTCAAACGCGTATCAGAATGTTTACCCTTTTTTTTTTTTACCACAG
ATCAAATGAATGTTTCGACCTAATGCTCCGTTTCGGCCTCCTAGACCAATAAAGGGGGGTGTTGCGG
TGGTGCAGAAAGTAGTAAACGAAATTTGCCACTACCACCAATCCTAAACCTGCAAAGATTTTGA
CTACCGATCCCGGCTCAACAAAATACGTGATCCAATGGAGAAAGAAAACCTTCAAAGAAGAACAAAA
CATGGGACGGTGATGGGTATGCCGTGATTAACAGCTTGAGAATGGGGCATGCGAGATATCTATCA
AGAACTCTGATGGCAAACTATGGGGAAAAGAGTGTTTACTGCGACACCTAACCTTGACGACGTGA
TTAGTGTGGGACCCTATGAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCCAGACAG
TGACACGTGTTACCCACCAGTTCAAAAAGTTGCTCCTCCACAGCTAGTAGTCGGAACCGCTTT
ATGACGACTGTGCCGATGCCATCGCGTTGCCTCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA
ATATCGATCCACATTTGGCAAAAGTGCTTCGTCCGCATCAGGTTGAAGGTGTGAAGTTTATGTATG
AGTGTTTAATGGGGTACCGTGGGTTTGGCGGGCACGGGTGTTTGTAGCAGATGAAATGGGGTTGG
GGAAACGTTGATGACAATCACTACAATCTGGACGTTGCTCAAACAAAACCCGTTTATGGAAAAAG
GTGCAGTGGTAAATAAGGTATTGGTGGTGTGCTGTACGCTTATTTCCAATTGGAGACAGGAGT
TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTGTTGACGCTCAACAACCCAAATGTCAAACGAGA
AACAGGATATACTCAATTTTGGAAAGTTGAATGTGTACCAAGTGTTAGTGGTGAATTATGAAAAAC
TTGTGGCACATTTTGTATGAATCTCAGCGGTCAAGTTTGATTGTAGTGTGTGACGAGGGCCATC
GTTTGAAGAATAGTGCAAATAAAGTATTGAATAATCTTATCAAGCTCAATATTTCCGAAGAAAATTG
TTTTGACGGGTACGCCGATTCAAAACGAGTTGGTAGAGTTTCAACGTTGATCTCGTTTCTCAACC
CGGGTGTGCTTCCCAGCTAAAATTTGTTTACGCGAACTTTATAACACCTATATCTAGGGCCCGAG
ATATCAACTGTTTTTGACCCTGAAGTGAAGAAACGCGGTGAAGAGATATCGCAGCAGTTGATTGAAT
TGACTCAGAGTTTTATTCTTAGACGTACACAAGCGATTTTGGCTAATTACTTGACACAGAAAACCTG
ACATTTTGTGTTTGTTCACCTACATCGTTGCAGCTCAAGTTGTTTCGACTATATAACCAACTTGA
AGAAATTTAATCAGTTTGAGGCATTTACCATGATCAATTTGTTTAAAAAGATTTGCAATTTCCCTT
CGTTGTTGGCCGACGACGAGTTATTTAAAAAGATTGTTGAAGAAAAGTTTAAATTTGGGGATGGCAT
CCGGTAAAATAAACATTTCTGTGCCGTTGCTATTGGAAATTGCTTCGCTTGGGGAAAAGATTGTCT
TAATTTCCAACCTACACCAAGACTTTGGACTTGTGGAACAGGTTTTGCGCAAGGTCAGCCTAACAT
TTTCGAGATTAGATGGGTGACCCCAACAATGTGCGTAGCAAGTTGGTTAATCAGTTTAACACGA
ACCCCGACATAAACGTATTTTATGTCGTGAAATCTGGCGGGATGGGGATCAACTTGGTTCGGGG
CTTCGAGGTTGATTTTGTGTTGACAATGACTGGAACCCAGCGACCGATTTGCAATCGATGTGCGGAA
TTCACAGAGACGGACAATTGAAACCGTGTTCATTTATAGGCTATTCACCACGGGGTGTATTGACG
AGAAAATCTTTTCAGCGACAGCTCGTGAAGAACAAATTGAGTTCCAAGTTTTTGGACAATGACGCCA
CGTCCAAATCTGATGTGTTTGAACAATGATGATTGAAGAATATTTTGGAGATAGATACATCGACAA
TATCCAATACTCATGATTTATTAGAGTGTGTGTGTGAGGGCGACGGGTGATGTTGAGTCAGCCAA
CCATGAGGAAAGCGAACCACCCCAAAACAGCATGGGTACTGCATTAGAGCTTAAAGAAGAAGA
TTGACGATGGTGAGGCGCTAAAGAGGACGGGTGTTAAATTTGCCTTGAACGATTATGACACTACA
ATCCAGAGGTGAACCGTAATTTGGATTTTGATTCTGCGCTACACCGAATTGCTAACAATTCAAGCT
ATGAAAATAAGCAATTGCCAATTACATTTATAATGCTGAGAGTAACTAATTAA

YBR073W_homolog 796aa (SEQ ID NO 294)

MFTLFFFTTDQMNVRPNAPFRPPRPPIKGGVAVVQVVKRKLPTTNPKPAKILTTDPGSTKYVIQW
RKKTSKKNKTWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADAIALPPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTTIWTLLKQNPFMKEGAVVNKVLVVCVPV
TLISNWRQEFRKWLKANKLVNLTLNNPMSNEKQDILNFGKLVYQVLVVNYEKLVAHFDELSAVKF
DLLVCDGHRHLKNSANKVLNLIKLNIKKIVLTGTPIQNELVEFHTLISFLNPGVLPKLFQORN
FITPISRARDINCFDPEVKKRGEIISQQLIELTQSFILRRTQAILANYLTQKTDILLFVPPTSLQL
KLFDYITNLKKFNQFEAFMINLFFKKICNSPSLLADDELFFKKIVEEFNLGMASGKINILVPLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVSLETSRLDGSTPNNVRSKLVNQFNTPDINVFLLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMSRIHRDQGLKPCFIYRLFTTGCIDEKIFQRQLVKNKL
SSKFLDNDATSKSDVFDNDLKNIFEIDTSTISNTHDLECVCEGDGSMLSQPTIEESEPPPKQAW
VTALELKKKIDDGEALKRTAVKFALNDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

AAAGAATTTCAAATTTAGTTTTAGGTGATAATTATCGTTCGTCCTTTCCTAACCTACCAATTTTGA
CTTTGTGTACTCATACGATGGTTGTTATTAGTTAAAGTTGCTTTGCTTTGCTTTTCAATTTCAATT
TCACAATTGAATTTCAGAATAGAATTAGTTTCACCTTTTCTTACAATCGGCTAAGATTTTTTTTCA
TTCTTCTAATTTAGTTTACAGAATAGAAAGAATAGTTTGCTTGTTGCTCATATTTACAATCAATT
GGTTATTGGTGTTTATTATTTTTTTTTTGGTTCCTCTTTTTACCCCCCTTCCGTCTAATTGAGTTA
TTGTTTGAATAAATTTATTACTTATTCAATATTTTTTTTCTTCTTCCCTTCTTCAACTTCTTC
TTTATACATTTTCAATCAACCTTCCAACAATCCTATAAATTACTTACTTACCTTCTTCAATTGGATTA
ATTGGATTTGAATTGTTACAATTGAATACTTCAACGAGATGACTTTACCAATTCAGGATTTAGAAC
CTGATTATTATATTTCCGTCAATTATCCTACCACCGATAATGGATCACCAACCCCAAGCTGAAA
AATCAATTGAAAACATTAATTGATTATTATACGATAAAGGGTTTGCCGCCCAAATTAGACCTGGTG
ATTTAGACCATTTGTTAGTCTTTGTTAAATTGTCTTCATACAAGTTTCTGAAGAAGCTGAAAAAG
ATTTAATTAATAAATTATGAATTTGGTGTCACGGGTAAAGATGACGTGTTAGCTTCTAACTTAGAA
TTATTATCAATACTTAACTTATCCACAATCAGTTGGTGGATGTGGTATTACTCCTAATCTGGGG
ATTGAAAATTTGTCAACGATATTGTTCCAATTACTAATGCCTTTAATGAAACCACTTTAGTTGAAG
ATTTAAAAATTAATGTTACTCAACCAAATTTATCAATTGCCACTATCAAAAAGACATATGGAGTTG
AAGTTGCTCTTTATTTTGAATATATAAAACATTACACTTTTTGGTTATTATTGCTTTCTATTATTG
GTCTTGTATCTCATTTTAGAAAAGATAAACGATTCTGTAACTTTTGCCTTTATCAATTTGCTTT
GGGGGGTTTATTTCTTGCATCATGGCATAGAAGAGAACAACATTTGGTTAATGTATGGGGTGTTT
AAAATAGTCATTTAATTGAAGAACATAATTCCGAATTGGCTAAAGTCAATGAAAGATATGAAGAAA
AATCAACTTATTTCCATGCAAATAATACCAATGGATTAGATTTTAAAAACAATTGGCATTATATCC
CCATTGCCTTGGTGTTTGGTGGTGTGTTGATTAGTTATCAATTGAGTTGTTCTGTATTGAAATCT
TTTTAACCAGATATTTATGATGGCCCCGGGAAATCTTTATTGACTTTATTACCAACGGTTTTAATCA
GTGTATTTGTGCCAATTTTGACCATTTGTTTATAATGCTGTCACGGATATTATTATTAAATGGGAAA
ATCATGATAACCAATATAGCAAAAATAATTCTATTCTTGTTAAACCTTTGTGTTGAATTTCTTGA
CTGGTTATGTTCCATTAATCATCACTTCATTCATATATTTACCATTTGCTCATTTGGTGCAACCTC
ATTTAGGTGATATTAATAACCACTATTGCCACATATGCTGGTGAATAAGATTTCTACACCAATACT
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ATTTCAATTGTCAAAATCAAGTTATACAATTGGTATTGAAATATATTCTCCCATTTGGGTTAAGAT
TTGTATTTAATTTTATTGAAACGAAAATTCAGAAGAAACCTCAATTACAAACTAAAGATGATAACC
CTGATGAATCTATTTGGTTACATAATGTCAGATTATCGTTGAAACTTCTGAATATAATGTTGATG
ATGATTTTAGAGGATTAGTTTTACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG
CACCATTGGTTTGTATTATTTTCAATTTAATTTTTTTTCAAGTTGGATAATTTTAAATTATTGAATG
GTAAATATTTCAAACCACCAAGTTCCAAGAAGAGTTGATTCTATTTCATCCATGGAATTTAGCCCTTT
TCTTGTAGCATGGATTGGATCAATTATTTCCCCCGTGGTACGGCATTTTACCGTCATGGTACTG
CTCCACCAAAATCTATGGGTCAATTTGCCCTGATAAAGCTAGTGTTCATGTTTCATCCTCAGTTT
TCTTGGTTTATTAATGTTTGTTCAGAACATGGATTTTTTGATTTTGAGTTATCTTTTATTGAAT
TCTCTTCTTTGTTCAAGAGTCAAGTTGAATGGGAAAATGATTTTGTGATAATGATATTAATTTGA
GACATGATTATTATTCTGGGAAAGTAAAACCAACTTATAAAGTCCACTCGGATGAGTTGTGGGAGA
AGTTTACCCCAACATCAACTTTGAATTTCACTGGTCTTAAACCAACCGCAGAACTGATGATAAAG
TTGAAAAAATTGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTACTGCTA
CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

MTLP IQDLEPDYYISVNYPTTDNGSPTPQAEKSLKTLIDLLYDKGFQAAQIRPGDLLHLLVFKLSS
YKFSEEA EKDLIKNYEFGVTGKDDVLASKLR I IYQYLTPQSVGGCGITPNSGDWKFVTSIVPITN
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVFLASWHRREQHLVNVWGVQNSHLIEHNSELAKVNERVEEKSTYFHANNNTNGF
RFLKQLAFIPIALVFVGVLSYQLSCFCIEIFLTDIYDGP GKSLTLLPTVLISVFPILTIVYNA
VTDII IKWENHDNQYSKNNSILVKTFVLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA
GENRFYTKYLLKLKSQEEFKINQGR LDAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKI QKK
PQLQTKDDNPDESIWLHNVRLSLKLPEYNVDDDFRGLVLQFGYLMFGPVWPLAPLVCIIIFNLIFF
KLDNFKLLNGKYFKPPVPRRVD SIHPWNLALFLLAWIGSII SPVVTAFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFK SQVEWENDFVDNDIKLRHDYYS GKVKPTY
KVHSDDELWEKFT PQSTLNFTGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS:
399..1781 (SEQ ID NO 297)

CGGTAATTATGTCAAAAAACAAACAATCAACATATTAAATCGTTATCCCAACTTTTGTCTAGTTT
CTAACACCTTTTATTTTGTGTATACAAATTGCACAATCAATTACTATAACTTTTTTTTGAAACGT
GGGCTCTGTTTAGTTTAACTTCTGTAGTTTATTATTCCGATTGGGTAGCTCAATAACTGCATT
TCGTACAATAATGTTAATCAATTCTAAATCCGATGAACCGAACACACAAAAACATCCAGTCTCT
GGAGAGATTTTTCAAAACTTCTATTATAAATAGAACCCCTATAAGTCCATAATAATCAATTGAAGG
ATTATTTTCTTTTCCCTTTTCTGATTACTTTACCAATTTTCTTCTCTCCAAAAAACACCTTCT
TCATGGTTTCTGTTTCTAAATTAATCAATAACGGGTGTTATTAAGTAGTCAAAGTGTTCCTCAAG
ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAATATACTCAATTTTCTTGGCGGTAGTG
CCCCTTATATTCAAAGAAACGGATATGGGATTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTC
AAATTCAATTGTATTCAAGACATGGTGAAAGATACCCAAGTAAAGTAATGGTAAAAGTTTAGAAG
CAATTTATGCTAAATTTGAAACTACAAAGGTAATTTAAAGGTGATTTGTCATTCTTAAATGATT
ACACTTATTTTGTCAAAAGACCAGAGTAACATAGTAAGGAACTAGCCCAAAAAATTCGAAGGAA
CCTATGCCGGTACAACCAATGCCCTTGCGTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT
ACAAGGAAACTCAACTTTACCAATCTTCACATCCAATTCTAACAGAGTACATGAACTTCAAAGT
ATTTGCTAGAGGGTTTGTAGGTGATGATTATGAAGAAGGTAAGTGTCAAGTTTAACATCATCT
CTGAAGATGCTGATCTTGGTGCCAATAGTTTGACTCCTAGAAAGTGCATGTTCCAAGAACAAAGAAC
TGAGCAGTAGTACTGCCAAAAAATATAACACAACATATTTAAATGCTATTGCTGAAAGATTAGTTA
AACCACCCAGGTTTGAATTTGACTACAAGTGATGTCAACAATTTATTCAAGTTGGTGTGCTTATG
AAATCAACGTCAGAGGAAGTTCACCAATCTGTGATTATTACCAATGAAGAATTCATTGAAGAACT
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GTTCAAGTATTTTGAATTCATCCTTGGAACCTTTGAAGGACACTAAGAACTCTAATCAAGTATGGT
TATCATTGCTCATGATACTGATTGGAATTTTCCATTCTGCTTTAGGATTATTGGAACAGCTG
AAGATTTACCAACATCTTACATCCCATTCCCTAACCCATACGTCCATTCTTCTATTGTTCCACAAG
GTGCCAGAAATATACACAGAAAACTTCAATGTGGAACGATGCTTATGTTAGATACATTATCAACG
ATGCTGTCGTGCCAATTCAAAAATGTGCTACTGGTCCAGGGTCTCTTGTAACTTGATGATTTTG
AAAAATTTGTTAAAGAAAGAAATGGAGATGTTGACTTTGTTAAACAATGTGGTGTCAATAGTACCT
ACCATCTGAGCTTACTTTCTACTGGGATTATAAAAAATGTCACTTACAGTGCTCCTTTAGAATTGT
AA

YBR093C_homolog_1 461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNQYGISTDIPAGCEIAQ
IQLYSRHGERYPKSNKGSLEAIYAKFENYKGTFGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKSSSTAKKYNTTYLNAIAERLVKPNPGLNLTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLLELLKDTKNSNQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYPFPNPVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
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YBR093C_homolog_2 1871bp public: 1..1752, PathoSeq: 1753..1871;
CDS: 501..1868 (SEQ ID NO 299)

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GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACCTTTATATCTTGGTGTGGGATGGTGCCACA
AATGGAGATTGTTGAGTGACATGAAAAATACGTAGTTAAATTTTGTTCCTGTTTTTATTATTTA
GCCACTTTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA
AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAAATTACGGGGATTTAATTTCG
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AAGCTTTCATAATAAACATAAATCTTTCCAGACAACATAAATGGTTGGTTTATCACGAGTACTTAATG
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AACAAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAAATTCAGGGTATGGGA
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AATTTTCATGGAGATTTATCTTTTTTAAATGACTATGAGTATTTTCGTTACTAATCCAGATTATTATG
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GAGCTTATTTTAAAGAAAGATATCAATCATTATTGACCAAAAGGAGAAGCTTGTGTGTTTACTA
GTAATTTCTGGAAGGTGTTATCAAAGTGGTGTCTATTTCGCTCGAGGATTTTATAGGAGATGATTACT
CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAATGGGTGGTAATTCATTGACAC
CAAGATACGCTTGTAACAACTTTGAATCAAGATTTACACAAAGATTTGGTGAATCAGTACGATAAGA
CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC
AGGTCTCGTCATTATTTCTTTGGTGTGCTTTTGAGATTAACGTTAGGGGGTATTCTCCATTCTGCA
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TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGATTGACAT
CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCGTTGATCGAGTACCATTTCCCAATCCATATA
ATGCAGCAGAATTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATTGAAATGTGGTGAAAAGC
AATATGTTAGATTTATTGTGAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGTCCTGGGT
TTACTTGTGAATTGAATGATTTTATCAAATTAGTTAAAGTCGTTTACATGATGTTGACTATAAGC
TTCAATGTGAAGTGGACGGACCGGAATTGACATTTTATTGGGATTATAAAGACAGAAAGTATA
ATGCGCCGTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)

MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMISRHGERFPKSGDGKYFNSVMEVFVKRYGEFHGDLNFLNDYEFVTPNDYEEKETPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNSGRCYQSGVYFARGFLGDDYSEDTFEVVVD
KKMGGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDNPLDLSADQVSSLFLWCAFEI
NVRGYSFPCNLFTKDEFIRSGYRNDVGNYYQTGPNNMTKVIGSPMVEASLKMQLQEDSKIWLTFTH
DTDLEMYLTSGLLIVPPGDLFVDRVFPFPNPNYNAEFFPQGARTYTEKLKCGEKQYVRFIVNDAVYP
YPDCSGGPGFTCELNDFIKLVKSRLHDVDYKLQCEVDGPAELTFYWDYKDRKYNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888;
CDS: 500..1885 (SEQ ID NO 301)

TGTAATATAAATAAGGGTATGAAATACCAACATCCCAGAATATCAACGAGATAGAAGAGAGGAGTT
TCAATATATATCTTGTGAATAATAACTTCGTTCTAATTCATATACACAACTAGACGTGTACACGC
TCAATCTCAGGTAAAGAAAGTTTATATTCATCTACTATATAACAACAATCAGGCTTTGCAAAAAA
CATTTAAAACTAATACTGGTAATATGGAAATATAACGCCCTCGTAGTTCTACGCACGTGGCATCCTT
TATCTATTTATTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG
CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAT
AAAAATAAAGTAATATAAATAGGTATGCATTTTCCCTACATTTATTTCTCTTTCTATTTTAAATTTG
TTTCTTAAACAGCAACAACAACAATTGAAAATTCAAAAATGGTTTCTGTTTCTAAATTTATTGAACAA
TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA
ACAATATAACATACGTCATTTCTTGGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGAT
TTCTACTGATATCCCTGCTGGTTGTGAAATGTCTCAAATTTGATTTCAAGACATGGTGAAAG
ATACCCAAGTAAAGTAATGGTAAAGTTTAGAAGCAATTTATGCTAAATTTGAAAACACAAAGG
TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTATACTTATTTTGTACTGATAAAAAACAATTA
CGAAAAGGAACTAGCCCAAAAAATCTGAAGGAACCTATGCCGGTACAACCAATGCCCTTGCGTCA
CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTC AACATTACCAGTTTTCTC
TTCCAATTCAGGTAGATGTTACCAAACTTCAAGATATTTTGCTAGAGGATTTTATAGGTGATGACTT
TAAAGAAGGTAAACTGTCAAGTTTAACATCATTTCTGAAGATGCTGATGTTGGTGCCAATAGTTT

GACTCCAAGAAGTGCATGTTCCAAGAACAAAGAACGGAGCAGTAGTACTGCCAAAAAATATAACAC
AACATATTTAAATGCTATCACTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAAG
TGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTCTG
TGATTTATTACCAATGAAGAGTTTATCAAATATTCTTATGGTAATGACCTTTCCAATTATTATTC
TAATGGTGTGCTGGTAACAATTACACCAGAATCATTGGTTCAGTGATTTTAAATTTCTTTAGAACT
TTTAAAAGACACTAAAACTCTAATCAAGTATGGTTATCATTGCTCATGATACTGATTTAGAAAT
TTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCCC
TAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAATG
TGGAAACGATGCTTATGTTAGATACATTATCAACGATGCTGTGCTGCCAATTTCCAAAATGTGCTAC
TGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATGT
TGACTTTGTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATTA
TAAAAATGTCACCTACAATGCTCCTTTAGGTGATTTTTAA

YBR093C_homolog_3 462aa (SEQ ID NO 302)

MVSVSKLLNGLLLAGQSVFQDVATPQQASVQYQYNIVNSLGGSSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPKSNKSLKAIYAKFENYKGTGKDLAFLNDYTYFVTDKNNYEKETSPKNSEGT
YAGTTNALRHGAAPRAKYGSYKENSTLPVSSNSGRCYQTSRYFARGFLGDDFKEGKTVKFNIIIS
EDADVANSITPRSAKSKNKERSSTAKKYNITLNAITERLVKPNPGLNLTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKYSYGNLDSNYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLIFHSALGLLEPAEDLPTSYIPFPNPVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYNAPLGDF

YBR093C_homolog_4 1886bp PathoSeq: 1..102/1038..1062/1078..1886,
public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303)

ACTACTTAAATTGGCATATCCAAACAACTTGAAGTAGGAGTTTCCTTATTTTTATTTTGTATTTA
TATATTTGATTGCGATTAATGTCATAAATTTTAGTTCGGTAATTATGTCACAAAAACAAACAATCA
ACATATTAAATCGTTATCCCAACTTTGTTCAGTTTACTAACACCTTTTATTTTGTGTATACAAAT
TGCACAATCAATTACTATAACTTTTTTTTGAACGTGGGCTCTGTTTAGTTTAACTTCTTGTAGTT
TTATTATTCGGATTGGGTTAGCTCAATAACTGCATTTTCGTACAATAATGTTAATTCAATTCTAAAT
TCCGATGAACCGAACACACAAAAACATCCAGTTCTGGAGAGATTTTTTCAAACCTTCTATTATAAA
TAGAACCCCTATAAGTCCATAATAATTCAATTGAAGGATTATTTCTTTTCCCTTTTCTGATTACTT
TCACCAATTTTCTTCTCTCCAAAAAAACACCTTCTTCATGGTTTCTGTTTCTAAATTAATCAATA
ACGGGTTGTTATTAAGTCAAGTGTTCCTCAAGATGTTGCTACTCCGCAACAAGCTTCTGTGC
AACATATAATCACTCAATTTTCTGGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGA
TTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAAATCAATTGTAAGTCAAGACATGGTGA
GATTCCCAACAGCAAGTAGTGGGAAAGATTATGAGAAAATTTATGCTAAATTTAAAACTACAATG
GTACATTCAAAGGTGATTTGTCAATCTTAAATGATTACACTTATTTTGTCAAAGACCAGAGTAACT
ATGCTAAGGAACTAGCCCAAAAAATTCCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTC
ATGGTGTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAACTCAACTTTACCAATCTTCA
CATCCAATTTCAACAGAGTACATGAACTTCAAAGTATTTTCGCTAGAGGGTTTTTAGGTGATGATT
ATGAAGAAGGTAAAACGTCAAGTTTAAACATCATCTCTGAAGATGCTGATCTTGGTGCCAATAGTT
TGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAACTGAGCAGTAGTACTGCCAAAAAATATAACA
CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAA
GTGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTCT
GTGATTTATTCACCAATGAAGAATTCATTAAGAATCTTATGGTAATGATCTTTCCAAATATTATT
CTAATGGTGTGTTAATAATTACACCAGAATCATTTGGTTCAGTGATTTTGAATTCATCCTTGGAAC
TTTTAAAAGACACCGAGAATCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAA
TTTTCCATTCTGCTTTAGGATTATTGGAACAGCTGAAGATTTACCAACATCTTACATCCCATTCC
CTAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAAT
GTGGAACGATGCTTATGTTAGATACATTATCAACGATGCTGTGCTGCCAATTTCCAAAATGTGCTA
CTGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATG
TTGACTTTTATTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATT
ATAAAAATGTCACCTACAATGCTCCTTTAGAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSNNQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYPFPNPVYHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFIKQCGVNSTYPSELTFYWDYKNVTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq:
939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632
(SEQ ID NO 305)

ATATATATATATTTATGTATTTTTTTTATTGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA
TAATCTATGAACAAATTAAAGAACTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA
TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTGTTGTGCGAATAGTTAGCGTAATAATC
TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTTCTTCTCGCACATATTTTATTAGAGCTTAC
AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTCGCACGC
TGTGGAAGGAGAACTTCACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA
AAAAATTATCAAATTTTCAACCTTGAGAGAAAAAAGTGGAAAAAACTTCTTCTTACATTT
AGTTAATTTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT
ATCAGTGATTATAATTAGAGTCTTTATTTGGATATTGCAATAATTGGATAATAAGAAAGAGCATA
AGAGTAGGAGTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTTATCGTCGTGATTA
TAACAAATACAAAGAAATTAAGCAATGAAGTGATATAAGCAAATGAAGGACTAGTTTATTAGGGGT
GACATTTTTTAGACTACGTAAAGTACTTTTCGATTCAAGGAAAACCAAATTTTAGTATCTATCAACA
AACTACAAATCAATTTAGTTAACTTCAATAATGACAATAATTTAATCACTGAAAACAATAAACAT
GCAAACAAGCAAACTAGTCAAGCTTTACGAATCAGTCAATACTAACAACTATTTTTTTTGTTCAT
TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA
AAATTACGTGTTTTCTACGGAAAAAAGAAATGGGTCAAGAAAGTTGAAGGTGACTCAGTTGGAGATGAA
TTCAAAGGTTACATCTTCAAATCACTGGTGGTAACGATAAAACAAGGTGTCCCAATGAAACAAGGT
GTTATGCACCCAACCAGAGTTAGATTATTATTATCTAAAGGTCACTCTTGTTACAGACCAAGAAGA
ACTGGTGAAAGAAAAAGAAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTTGTCAGTTTTGGCT
TTGTCCTATTGTTAAACAAGGTGACAAATGAAATTGAAGGATTAAGTACACCACTGTTCCAAAAAGA
TTAGGTCCAAAGAGAGCTAACACATTAGAAAATCTTTTGGTTTAACTAAAGAAGATGATGTTAGA
GATTTCTGTTGTTAGAAGAGAAGTTACTAAAGGTGACAAAACCTTACACCAAGCTCCAAAGATTCAA
AGATTAGTTACTCCACAACTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAGTCAAGAAATGCT
CAACAACAAAGAGATGCTGCTGCTGAATACGCTCAATTGTTGGCTAAGAGATTGCATGAAAGAAAA
GAAGAAAGAGCTGAAATTAAGAAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)
MKLNISYPANGTQKSMIDDDTKLRVSTEKRMGQVEGDSVGDEFKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCIVAQDLSVLALSIVKQGDNEIEGLTDTTPVKR
LGPKRANHIRKFGLTKEDDVRFVVRREVTKGDKTYTKAPKIQRLVTPQTLQRKRALKAKKVKNA
QQQRDAAAEYAQLLAKRLHERKEERAIEIKKKRAESLKN

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;
CDS 501..1517 (SEQ ID NO 307)

GTGACGAGAACTTCTGTCTATCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAACAAT
GATAACGGAGGAGGATTATCCCATACAAACAGAATAGTTGTTGGTGATGTTGTTGGGGTTGGTGGT
TCTATATTAAATGGTTTGTGGCCGTTTTATTTTACTTTGAGAAAGAGAAACAACCGTGATTATGAA
GGTGGATGGACTTTCTGGAGAAAGAATGAGAAATTTGGGAAGTGATGAGTCTTCAATGGTGAAATTG
GGTGTCTAGAGACAGAAATATTAATCAAGGATCAAATTTTTAAACAAGGCTTATTTTGGATGAGGGT
GGTTTTTTTTTATAAGTATTTTGTAGTTGAATTTAAATTTTGTACCTTAAAGTCTTTTAAATTTAAT
TTTAATAAAAAGTGGTGATTTGGCAAACCTTCAAGAGTATATTTGGTGAAAAAATTTTGAATTTG
GAAGTGAACGCGTCTAACATCTTATACCTCTAAGCAAAATGTCAGAGTACTCTGTGTATCAACAGT
TGAATGAAGATACAAACGCAACTAAATATACTTATAAATTACTACAGCTACCATCAAAGATACTAA
ATCAACTTGAATCCAAGTCAACTAACTTGTATATAAATCTGATATCAATTCCTTAGCATTATGCA
CTGATTTCAGAACTTTCAAGTTACGACAAATGAACCATTCCAATACAGTCTTGCTATTGAACAAAG

AACCTGACAACAAGTTAATTGGGTTTCAGAAAACCAGTTATGAATATGAGTTGACAGAAATCAAAG
GTTTCGATCGATACGTCCGATATCCCTATTTTCAACGGACAAACAGCACAGCAACCTATTGATTTGA
TAGCATTGGAAGATAATTTCGATTTGTTTCACATCAAGAGTTTTTATCGAATTGGTATGAGTTGGGAG
GTTGTGAAATTGATAAATGGAGCATATATAATGAGTGCAGATATTATTACTGAACTATTATATCTAT
TAATCACCAAATTGATGAGTTTACAAGTGCACGAGTTTTCTCCGGAAGATGTTTCATCCATCATCA
CGCCCCCTTATAATGACTCAATGGTAACATCAATCATAACAAAATTTTGCACATATAGAAAGTGAGA
AATATCAATTGAATGATTTAAAAATTACACAGTGGTTTGGCATTGTTGAGATGTCAAAAATCAATC
ATAAAATGACCGATATTTTCAGAGTTCCTATTGAATTGGAAAACCTAGTTTGCCGTCATTCTATAACC
CTCCATTGGACATCAGTCAATTGGCAGGCTATTACTGCTCCCCAATCGAAAACAAAATATTGTATG
TCGACCCAGAATCTTTATCAGAAAATTTGAGTCAACGATTCAAAGAATTGTTTGAATTGGATAAAA
GTTGGAACCTATGATGAGTTTATTCCATTCATTAAAAAGTTTGTTCCTGCCGGTAAAAAGGTCGACT
CAATTATTTTAAAGTATGGCAAGAAGAAGAAAGTTGGTAGAGATAGATTTATAGTCTGTCTAGAT
AA

YCL016C_homolog 339aa (SEQ ID NO 308)

MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLQRMNH
SNTVLLLNKEPDNKLIGFQKTSYEYELTEIKGSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLIKLMSLQVHEFSPEDVSSIIPTPYNDMSMVTSSII
HKFCTIESEKQLNDLKITQWFGIVEMSKINHMKPTDISEFLLNWKTSLPSFYNPPLDISQLAGYYC
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

GGTGGGGTCCCATTTTAATTTAAAAAAATTTTTTACCATCCAAAGGATTTTATTTACCCAAAGAC
CAAAAAATTATTATTTGAAATGGGGATTAAATGGGGATAATTTTATTTGCGCTGATGAAAAGATT
AGTACCCGTTTGAAAGTCCTGATTCAAATTTATGGTCAAGCTAAAAGAGAAAATTTTGATTTAATTA
CTGGTGATAAAAAACCAAGAATTTTCCATGTTGATGAATCATTAATTGATGATTTCTCAAGAAGCTG
CTGATGAATATGAAAAACAATTGATTAATAATTTTGCTAAAAAAGATTCCGGTGAAATTACCTTTAT
TTGATTTATTTTTATTAGGTTGTGCACCGGATGGTCATATTGCTTCATTATTTCCCTAATCATGGTG
AACAAATTGAGAGAAAAATTAGCTTGGGTTTACCAGTATCAAATGCTCCTCTGGGACCAGAAAATA
GAATAAGCTTTATCTATCCAGTTATATGTCATTCGCCAAGAGTGACATTTGTTGTTGAAGGGTTAA
CTAAGCACCAATTATTAAAAACCATTTATGGAAAGACCAGAAAAGGTTTACCAAGTTCAATTGTTA
ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTTGTGTTGATGATGCATTGAATGATTTGTTTGATA
TAACTAAAAAGAAATACAAATATTTATCTATACCTGAACCAAGTCATTAA

YCR073WA_homolog 131aa (SEQ ID NO 310)

VKLPLFDLFLGCPDGHIALSFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICH SARVTF
VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSFVDDDALNDLFDITKKKYKLSIPEPSH

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TGTTACAAAACATTTCTGTTGGAGAGATAATTGAATTCAAATTAACGTGTTGAATCCAACATTGAA
CAATGAATACACGTCCAAGAAAAATTTGACATGATTAGAATCGCGGTCAATTACATTCCCGGAACG
TCTTGGACTACTTGGATACAACAATGGAAAAATGAGGAAAAATGAGGAAAACGAGGAAA
ACGAGGAAAAATTTTACCGAAGAGTAATTATATTACAAGCATTGAAAGAGGAGAAAGTGAACGCCCC
AAACAGAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAAATTTTGGTTCAGAA
CACAACCTTTGGGAAGAAAGAAAAAACCAGAAAAAGAAATTCATCTAAAACACATACACAATATAT
ATATATATATATAAATATATCCATATACATATGCTTTTAATTTAACCTTCCCGCCTTTCTTTTCTTC
TTTTTGAATTATATCGATTTTAAAACTACACTTCATCATGGCTGGAGTTAGACAATTAAGAATAA
TAGCATTAAACGGCCTTTGTCCTTGGTTTAATTTTTACTTTACATAAAGTTGGATCCAACGCTGCAT
CCTTGGTTCATGCACAAGCATCAGACCAACAACCAACATAACACCAAAAAGTACTACATATA
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTTGATTCTAAAAATGATCCTCAAACCTGATGACA
AAATGAATCAAAAAATATCACAAAGATCAAGATGAAGCCATCAATGGTAATAAAGACACATAATAAAG
ACACCACCAAGTCAAACCAGATAATGGTGAATATGATTCATCAATATCTGATTTGATAAAAATTAGAT
CATTATCACCAATGACAATTTTCAGTAAATCATATTGTCCATATTCAAAAAAGATTAAACAATTGT

TATTAGAAAAATATGATATAACACCAGCACCAAATGTTGTTGAATTAGATCGATATGAATATGGAG
CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAAGAACTGTGCCAAACGTATTGGTTGGTA
AATCATTTTGAAGTAGGGGTGGTTGTGATGAATTTGAAAACTTCATAAAGATAATGATTTGATTA
AATTGTTAGTTGAATGGGGTCTGGTCGTTTACAAGTTGCAAAGAAGAATACCCCATCAAATGCCT
AA

YDL010W_homolog 229aa (SEQ ID NO 312)

MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQQPNKHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKDTNKDTTKVKPDNGEYDPI SDLIKIRSLSPMTIFS KSYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTPVNVLVGKSFESRGGCDEFE
KLHKDNDLIKLLVEWGSRLQVAKKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1:

501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313)

AGTGGTTGTTCAATAATGGTAAGTTCCTGGAAATAGCCATTGTTGCTTCTGGTGGTTAGACTTGT
AGGAAGTAGAACTGTTTCCAATGAAAAGTAGTTTTAATTAGAAAAATTTCAAAGTGCCTGAAGC
CCAGTCTGAATGTGCGAGGAAGCCAGTCAGTTAGTAGTGTCTTCCCTCCACTGTCTGTAATACA
AAATTTCCCTTAGTGAAAATGCGAAATATATCTGTACTGGGAACCCCCCGGAAAAAAAAAACCTA
TGCTCAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAACTT
TAATATGGTGCGAAGAGCGTTTCCAATTTTTTTTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC
TGTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTTCAGAACAGGAAAATTTTTGAAAT
CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA
AACGAATTGAAATAAAGAGATAGAGAGATGTTTTATTATCAAAATACGAAAGGAAAGGCAATTAAA
AAAGGAAATCAAAAAGTCCCAACCTTGCAGTAGAAGAATTGAGGTATATGAATTTGATAGATAGCC
AGAACGGTGTTACATAAATGGGATATAGAACAAAACCTATACGAGGAGTTTGTTCACGATCATTC
AATAACCAGAAAACGATAATATTTAGCGACCATTAAATGACACTTGAAGGCTCACTGGGCCAATA
TAATATGGTCCATATACACTTTTGAACATTTTTTACTTAACAATTTACTTTTGTCTAGACTTTTGGA
AAAAGAAGACTGCCACTGCCGTTGCTCATGTTAAAGCCGGTAAAGGTTTAAATTAACGGTT
CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTTACGAACCATTGACTTTGGTTG
GTTTAGATAAATTCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG
TCTACGCCATCAGACAAGCTATTGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG
CTTCTAAGAACGAATTAAAGAAAATTTTCGCTTCTTACGATAAGACCTTGTTAGTTGCCGACTCAA
GAAGAATGGAACCAAAGAAATTCGGTGGTCTGTTGCCAGAGCAAGATTCAAAAATCTTACCGTT
AA

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)

MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVYEPLTLVGLDKFQGIDIRV
KVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEASKNELKKIFASYDKTLLVADSRMEPKKFGGRG
ARARFQKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGGTAAGATATAGAAAGCTTACCACCTTTGACAAGTTTGAAATAGGATGGGTGAAAATTTGGACAT
CTTGAATACTTAAAATTTCTGAACCTTGATCACCAGATCCTTTTCTTTTACATAATTAGATATGATGG
ATAGGTTAGAATCGTCTTTAAAGAGAAGGTATAATATCTAACTGATTTGGCGAGGTGTTGGAAAAG
TCACTCCACTGTATATATTCTCGGAGTTTAACGTACTACAGTTCAGTGGGGTGAATACCTAAATAG
GGGGGTAGAATACGAACTCCTACAAATTTTAAGGAGACTATGACCCGAAAAGAGAAGAAAAATTTA
TTACTCTAAGAACTTTATATACCTCCACAACACTCACTTTTCTTTAGTTTCATTCTGCTTTTTTTTT
CTTACACATCTTAAGGTCAAACAATTTAACTTATTAGCTTGTGAAAATCTCACTTCAATTCAAGTT
CTCTTTCAATTGACATTATAGTATTTCCCAATTC AATTATGGCTTCTCATGCTTCTGTATATTCT
GTAAAATTATCAAAGGTGAAATTCCTTCTTTCAAGTTAATTGAAACTGCAAAGACTTATTCCTTCT
TGGACATTCAACCAATTGCTGAAGCCCACGTTTTAATTATCCCTAAACACCATGGGGCAAAGTTGC
ACAACATTCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA
AATTGGACGAAAATAATACTCCAGAAGGTGAAGGTTATAACGTTTTACAGAACAACGGAAGAATTG
CTCATCAAGTTGTTGATCACGTTCACTTCCATTTGATTCTTAAAAAGGATGAGGCTACAGGTTTAG

GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGATAAATTAGGAAAATTGCATGAGAAATTAAAGG
AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)
MASHASCIFCKIIKGEIPSFKLIETAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNI PDDYLSDILP
VVKKLTQVKKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294
(SEQ ID NO 317)
CATAATTATTACATATAAACTCGCACTATAATTTTTTTTTTTCTATTCTGTGTGTGTGTGTGTGT
GAGAGCCAGAGAAACCAACTGACTGAGTGCCTCTCAACAATTTATTTCTCCTCGTCTTATT
TTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTA
CCAAAACACTAGTATTTCAACATGAGAGATAAGTGGAGAAAAAAGAGAGTTAGAAGATTAAAGAGA
AAGAGACGGAAGGTTAGAGCTAGATCCAAGTAA

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318)
MRDKWRKKRVRLKRKRVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1:
501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)
TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAAACTTATATTTGAAAGTAAATTCTA
TTATTTTCTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCATTGTGTGTGGAA
TAAATTTAAATCCTTCTTATTGGTGTCTAGACTTTGCTTTTTGTGGTGATTAGGGCTTTAGCCCT
ATCACGTGAAATACTGTATATAAAAAATCTTTATAGCGCGATAAAACATATTTTTTTTCCGTATT
AACAAATATGTGTGAAGTTTTGTCCTGGTGTTCCTCACTGTTTTCTTTCTTTCTGGTAGTAT
CAATTAACGCTTAGATCCAATACAGTTTGGTAACTTGTACACGAACAAAATCTCAAATTTGTTAC
TGTGTGAACCAACAAGGAAGAGAAAAAAAACCCATACAAAAATTTTTCAGTATCAAGGAATTAGA
AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTAATATCGATATTATCCA
TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCATTTTAT
TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC
CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAGTTTCAAGATACACGTAA
ATGAAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTGTTGGGTTTAGATTACTA
TATTTTACAGAAACATATTATATGAAATGATACCCAATCCACAGCGACTTTTCAGATAGCCAAAT
AACTAAGCAACTCAAGATAACATAGGATCATGCATCAATCAAAATGAAACATTAATACTAATAA
CTTTTTTTTTTATTTATTAGGCCGGTGTAAACTTTTCAATTAAGAACTAAATCTAAGGAACAATT
AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAGTTCAAAAATTACAAAGACC
AAGTTTACCAAGAATTCACACTGTTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAACTTGAA
TCAAAGAGAAAATGTTTCGTGCCTTTTACGCTGGTAAAAAATACATTCCAAAAGATTTAAGAGCTAA
AAAGACTAGAGCTTTAAGAAGAAAATTGACTAAATTTGAAGCTTCTCAAGAACTGAAAAAGCTAG
AAAACAAAGAATTGCTTTTCCACAAAGAAAATTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320)
MAGVKTFELRTKSKEQLESQVLVELKQELATLKVQKLQRPSPRIHTVRKNIARVLTVINLNQRENV
RAFYAGKKYIPKDLRAKKTRALRRKLTKEASQETEKARKQRIAFPQRKFAIKA

YDL167C_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:
501..2687 (SEQ ID NO 321)
CTCTGTGTAAATTGATGAAATCCACACAATAAAAAATTTCTTTCTTTCTTTTAAAGAACCTAAAAACA
GAATCAACATTATTTGCCCCATACATATCCAAGAATTAAATACTTATTAGTTCTAAGTGGAATAGA
AGAGAATCAAACCTTAACATTACTGTTACGCAACGTCAAGAGGGCATTTTTTTTAGTTTTAATTTGT
TTCATTTCAATTGAATCTTTAAGAATCACCGAGTATACATACTTTCTTTTGTATTTTATCAGGGAA
GCCACATCCAACCACAGTTACATCCCAAAAAATCCCTTAATCTTGTTCTTAGTTGTATTATTAAT
CTATTGAATTTAAGTTTGATATGCGAGAGAATATTGTGGATTGTATAAGTTTGAACCTGGACTTGA
ATACTTTGAGGGGCTTAATCATATATTGCATTTTATACCTACTCGCGGTGTTGCTTACCACACTG
ACTAGTATGATCTTTCTGAGATTTCTAGCCAATAAATTATGAGTGATATTTATATTATTATTCATA

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCTACTAAGGATTCTTCCGAGTTAATTGAATTTG
CTTGGGAAACAGTCGATAGTGTCACTTTGGAACTTTATACAAAGGATCAAACCTGGTTCGTCCAA
CCAACACACCTATCACACCTTACTGCTCGAAGATTCATAGAATAACATGGGACAATGTCAAAAATG
CTGGGTCTGTTCAAAGACGCCATCACAACTTTTGATCAATACGTACAAGAACACATAATTTCCAAGA
AAAAGGAGTTTTC AATTGTGATGTTTGACATTTCCAAATTGAGAGTTCAGTTGGTTCGTGAAGCTA
GAGACAAATCCGTGGTTTTACCTCGTATCTACAACATCCAAGGATTTTGTATTTACCAAGAGAAT
ATTTAAATTGGCAATCTAGCCACCCTGAAACATTATCATACCCCCCAACTTCTTTAACTAATATTA
TTACTGCATTAGAAGTTGAGGTGAGAATATATCTGAATATGTGCGACTTGCCAACTTTTCTTCCA
CACCATCACCATCAAAAGCTTCAGCAACAACGACGACGACAACCTGCAAAATGTCACAGCCATTGACG
TCCTTTCCAGTGAAACAGAACCAAAATGGTAAAGTCATTGCAAAATTTGCACGCCAAAATTGCCAAAC
AATTGATCAAAAAATCCATCCCTGTTGAGAATCACCCCTAATGTATTTACAAGACCTTTTGATTCCGG
CTCAAGATATCACTGCTTTTACATCAGAAAGATCAAAAGTACTCTATCTTTCCAACCTGCCAAACG
ACACCACACAATCAGAGTTGGAATCATGGTTCACCTCAGTATGGTGGAAGACCAGGTGGGTTTTGGA
CTTTTAAGTCTGCAGATGATAACAATAATAACAACAACAATAGCAATGGCGGGAAAGGATATC
AGAATGCGAGAAAATATGGTATTTT CAGGTTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT
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TGTTTGATATGGCCATGGATAAAATGTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC
CCGGGGATTGGACTTGTATCTTGTGGGTTTTCCAATTTCCAGAGAAGAACACACTGTTTTCAGGT
GCTCTTTTTCGGGCAGTGGCGTTTCAGGATGTTTTTAAACAGTAATACAGGCAATGCCAAGGTAATG
GCAATGTTAGCGGCAACCACAACCACAACCACAATAGTGAGCTCGCCGTGGCATGAATTTACAGC
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AGGGTCCAACAGGTAATGTCACTAATCACCTCAACAATTCTGAGACCAATTTACTGAACAACACTA
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ATAACAATCATGGGAATAGCAATGGTAACACCATACATGGTCGTTCCCAATTATAACAATAGTGTTT
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CATTTTTGAACCTTCAGCAACAACAGTCTCAGTCACAACCCCAAGGTCAGCACCATTACAACCAAC
ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCAAAGAATCAGT
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AAAATCAAATTTTGATGTATTCACAACAATTGCAACAACAACAGCAACAACAACAGCAACAACAGC
AACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACATGATTTAA
ATGGAAGTAGCTCTTCCCATCAACTGAACTTCAATTGAATAATACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)

MSDIYIIHISTTCDDSPFVTKDSELIEFAWETVDSVTLETLYKGSNLVRPTNTPITPYCSKIH
RITWDNVKNAGSFKDAITNFDQYVQEHII SKKKEFSIVMFDISKLRVQLVREARDKSVVLPSYLQH
PRIFDLPREYLNWQSSHPETLSYPPTS LTNIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTAIDVLSSETEPNGKVIANLHAKIAKQLIKSIPVENHNPVFTRPFD SAQDITAF TSERSK
VLYLSNLPNDTTQSELESWFTQYGGRPGGFWTFKSADDNNNNNNNNNSNGGKGYNARKYGISGFVA
FNTHEEAVDCLALNGRVLNDRPLEVQASSSKVDFDMAMDKLLLT SFPLSKNRPRPGDWTCLSCGFSN
FQRRTHCFRCSFAAVAFQDVFNSTGNANGNGNVSGNHNHNHNSGARRGMNLQPAQANEKIGTGNI
SIPSYNDPIKGPTGNVTNHLNNS ETNLNNNTNLNNNNHH SNNYHNHYHHNNNNNNHNSNGNTIH
GRSHYNSVPFRAGDWKCENCMYHNF AKNLCLCKGVAKPAINNQNNNTIHSVNSTAAAI AAATAS
GQPLNLNNNAFLNLQQQQSQSQPQGGHHYNQHSRNNNASGASKFNNGYNPKNQYYNNNSKNLSNNF
GLNGMHQQNQNLQILMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDLNGSSSSSHQSKLQL
NNT

YDR238C_homolog 3359bp public: 1..1467/1469..3040/3042..3359,

PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

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GGTTATATTTTAGCAGTTTATAGACAGTGTATCGATGGGTAATATAAAATAAAAGCTCATTGAATA
CTATCTAGTGAAAAGTCGTGTGTAAATCGATTTGAAAAATATAAAACCATACACGTAATGAAATG
TGTGTGAAAGTACAACCAACAACGAAAAAGAACAAAAAAAATGTTGTCCGCCAAAAAAAAG

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTGTGTCACCATAACTATCAATTGTTCA
CCTCTTGAACCAACATCAAAATTGAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG
ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAATGGAGACCCCTTACCTG
ACTTGTGTGATGCATATAATCAGATTTGTGCATGCCTTCCAGAAAATAAAGAAATTGAAAAAGTTGTTGT
ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAATAAGAGACATGAAATGATTCTTG
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ATTTGACGAAATTGAAAGAGCCAGAATTATTGGAACTTTAGTTCCTAATGTCCGTCAATGTTTAG
AACACCGTCATGCCTATGTCAGAAAAAATGCTGTTTTTCGCATTATGGTCTATTCATAAAGTCAGTG
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AGGACTCTATTCAAAATCCAGCTTTTAAAGCAACAATATGCCCAATTAATGACAGAAATTATTGAAA
GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT
CAATTTTGTGTCAGGAAACAAGTTTGTGTTGAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA
TTATCACTTTATGAGAGAATAAATCAATTACACAAGCAACATCCTGGTGTGTTACAAGACTTGTCAAT
TAGAAATTTTACGAGGTTTATCTTCCCAAGATTTGGATGTTAAAAAGAAAGCTCTTGATGTTACTT
TACAATTTATCAACACCAGAAATGTTGAAGATGTTGTTAAGTTATTGAAGAAAGAATTGCAGTCTA
CAGCTTTATCCAATGATGACAAGAATGCAGATTATAGACAGTTGTTAATTAATGCCATCCATCAAT
TGGCTATTAAATTTGTGGAGGTTGCTGCCAATGTCATTGATTATTGTTGGATTCTATAGCCGATT
TGAATACCACTGCCGCCTACGAGGTTATCACATTTGTTAAAGAAAGTTGTTGAGAAATTTCCAGATT
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TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTGACAAGCGAAACAACCTGACTCTTTGGAAA
GTGACAGCAAGACTCCTATCAGAAAGCAAATTTCTTGTCTGGTGATTCTTACTTACGATGATTATG
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ACGGATTAAAAGCAGAAGCATTGTTGATTATGGTTTCGATTTTAAGAGTTGGGGAATCTAGCTTGG
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TTATACAATTGACTGGGTTTTCGATCCTATTTACGCAGAGGCATTTGTCAAAGTTTCATCAATACG
ATGTTGTGTTAGATGTCTTGCTAGTGAATCAAACCACAACCTACTTTAAGAACTTATCAGTTGAAT
TTGCTACATTGGGTGATTTGAAAGTGGTTGATAAACCAACTACCGCAAATATTGGACCTCATGGTT
TCTACAAAGTTCAAACAACCTATTAAAGTTACTTCGGCTGATACTGGTGTCACTTTTGGTAACATAG
TGTATGACGGTCAACACTCGGACGATTCACGTATAGTTATTTTGAATGACGTTACGTTGACATTA
TGGATTACATTAAAGCCAGCCACTTGTTCAGAAAGTCAATTCCGTAAAAATGTGGAACGAATTTGAAT
GGGAGAATAAGATAACCATTAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA
AGGGTACAAATATGCAATGCTTGACACCGGGTGCAGTAATTGGAGAAGAAATGTCAATTTTTATCAG
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GTGATGGACCAATAATTGGTCATGTCAGAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTCAATTGG
GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTTTAA

YDR238C_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSVNEFNLEKKGDDVKVDTMKKILITILNGDPLPDLLMHIIRFVMP
RNKELKKLLYHYWEVCPKMDSESGKMRHEMILVCNAIQRDLOHPNEYIRGNTLRYLTKLKEPELLET
LVPNVRQCLEHRHAYVRKNAVFALWSIHKVS DHLPDADELIYRFLYEENDSVCKRNAFVCLGDLN
REAALQYIQDNISVIETLDPLIQLA FIEFIKKDSIQNPALKQQYAQLMTEIISSSNVVMYEAANT
LTVLTSNPQSILLAGNKFVELATRES DNNVKIITLERINQLHKQHPVLQDLSLEILRGLSSQDLD
VKKKALDVTLOFITTRNVEDVVKLLKELQSTALSNDKNADYRQLLINAIHQLAIKFVEVAANVI
DLLLDSIADLNTTAAAYEVITFVKEVVEKFPDLRDAILRLILALPHVKSGKVFRRGALWVIGEYALE
ESLIQESWKYIRGSIGEVPIIAS ELKSKRDDTEESQEEETEYDGKPRRKGPVVL PDGTYATESAL
TSETTDSLES DSKTPIRKQILAGDFYLGAVLASTLVKLILRLQSLKQTQEKILNGLKAEALLIMVS

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAEEALA
KDLHDNAEQIDDAIVFRQLDKDNKSKASVDDVAAAAGSNEELKKNLSSRLNKIIQLTGFSDPIYA
EAFVKVHQYDVVLDVLLVNQTTTTLRNLSVEFATLGDLKVVDKPTTANIGPHGFYKVQTTIKVTS
DTGVI FGNIVYDGHSDSRIVILNDVHVDIMDYIKPATCSESQFRKMWNEFEWENKITIKSPIET
LKEYLDELKMGTMQCLTPGAVIGECCQLSANLYSRSSFGEALANLCIEKQSDGPIIGHVRI
KGQGLALSLGDRVASISRKGGKATIARV

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;
CDS: 501..2267 (SEQ ID NO 325)

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TGTTTCCCGTATTGTTTAAAACCAAAGAAAAGGATAATCAAACTAAATCTTTCATATTAACACT
ACCATTTTGTAGTGGTCAGTTTATATAATTATCCACTGTTCTCTTCACAATTAACAAAAA
AAAGAAAAAGAAAGCTCTCTCTCCCCAAAAGAAAAGCAAAGGTAATTCCTTCATACACACCTT
TGATATCTTCTCTTAGACTTTTCTTTTAATACTTGCATCAATTGGAATATTACTTGTTCATACT
GGAGTTTTCATTGAATAAATATTATTAATAATTATTATGCTTGAATTGAATTCAATTACGATTC
CTCGGAATTTCACTGAATTCACACTCACAGCATTAAAGATCTACTATCAACTTAAGATTTTATTTT
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TTGTTGGCTATGTTGTATACACTCAATTATTAAAGCTTTATCGAGTATTAAGAGGGTACGGTATTG
TAGATTCTATTGCAAGGTTATACCTATATGTTAGTTCTACGGTGTCTCATCTCAAATCTTTTCACTAC
CATTTATTAAATCCAAAATTGACAAGGAATTGCAAGCGACTATTGGCAAAGTAGAAGAAGAGATTA
TGAAAACGATCCACAGTTATTACAGTTTCCCGAATTGCCAGAACAGGGTATTGACGCTGACAATG
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AAGTCATTGCCCCCGTGACAATACATGCGGAATTGAAAAGCCTGTTTTTATTTTGAATGAAAT
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GATTACAGGTGTCAGTCAATCTCATGTGATACTACAAAATATGGGTTTGTCTCCCAAGGGGTCAT
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CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTTGTTACGATATTGTGCTGGCGTCAA
TGAAAGTTAAACGAGCAATTGAACTGACCCGATACTATCCAAACATTTACAAATTATTGGTGATC
CAATTGGGTGCGTAATTTCTGTTCAACTTGCACCTCAGCAATCGGGAAATTTAAGTATTTACGAGA
TTAGTGATTTGTTGACCAAAAAAGGTTGGCATTTTGCAACTTTACAAAACCATCAGCATTACATT
TTGCATTTACAAGATTGACTGTCCCGTGGTTCGATGAATTGATTGCAGATTGGTTGAAGCTACAA
AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAGAATGGAGTGACCAAGCTCCAGGTGATACTG
CTGCGTTATATGGTATAGCTGGCAGTGATACATACAGCAGGGTTGGCTGATAGATTAATTGTTGCAT
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YDR294C_homolog 589aa (SEQ ID NO 326)

MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGYVVTYQLLKL
YRVLRGYIVDSIRRLYLIVSVSTVSSQIFSLPFIKSKIDKELQATIGKVEEIEIMKNDPQLLQFPEL
PEQGIDADNVSLDKLQNLKHSWDWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVFPVGV
RKMEAEEVHMLDIFNAPSDGCGSTTSGGTESLLLGLSAREYGKKYRGITEPEVIAPVTIHAGIE
KACFYFGMKLHKVDLPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGFSFIVSFLEKSKVHGDRKLPFDFRLPGVTSISCDTHKYGFAPKGSIIIMYRSPKLREC
QYYIASDWTGGMYSPTLAGSRPGALVVGWATLINIGKQGYTKFCYDIVSASMVKVRAIETDPIL
SKHLQIIGDPIGSVISFQLAPQQSGNLSIYEISDLLTKKGWHFATLQNPALHFAFTRLTPVPVDE
LIADLVEATKEAVAIAEEHKKNGVTKAPGDTAALYGIAGSVHTAGLADRLIVAFLDLTLYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public:
331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327)
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AAAACCTTCCTTTTCTGGTGATAAATTTTGACTTTGAAGCATAAAGAAGACAGAGCTAAAAA
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AAGAATCACTCCAACAAGTTTAAACTACATTATCAATTATGTTGAAAACCTAGATTAAACAAAGCA
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TCACTGCTGTATCATTAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCTTAATG
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TTTTAGAACATACAACCTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTTTAAATGA
CCAACAGGTCGTTGAGTAACTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG
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AATTAACCATACCGATTTCTTGCAAGAAGGATGGAGAATAGAAAATCAAAATGTTTCATGACATAT
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AGAAAATTGTTGATTTGCTGTACGAGGGTTTACTAGAGTTTCACCTGAAAAATTATCATCCATCAA
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ATGAATCATTCGAAAAAAGGTGTCTTCAGTTGACGTCAAACAACCTATATTTCTACAGATAAAT
CAGAAATCTTTGATGTCAACATCCCGGTCCAGTTGATACAATGAATGGTAAAAGAGACTTCGAAC
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AAATCATTAATAATAAAATCATTTCCCGAATTAAGTAACGAAGAGTCCTCTTCATATCATGGTAGAA
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ACAAGAAGGCAATCTATGAGCAAACTTGGAAATTAGCTAAATTACAATTGGAGGATCAAAATACAG
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CTGGCGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC
AGTATGTGTTAAGTGAATGGCTTTGAAAGAAAAGTCACTCCTCAGTTTATGATTTATGGTTGGAGA
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ACATGGGACAAAACCAATCAATAATATTGCTGATCGCGGTCAATCTTATGCGGCTGCTGTGAGCT
CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTCAGGTTTGGAGTCAAGTTCAATTTG
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TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAATCAAG
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GTGAAAATGTCCTTAGTTAACTTACCATTTCAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT
CGTATTCATCAAAGGATGGTGCTTCTTTACAAATATTATCTCAGTTATATTCTTTAAAAATCTAC
ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGCATATGATGGGTGAACGGGA
CATTAACCTTTTATTCGTATCGTGATCCTAATCCTGTTAAGTCGATTCAAACCTTTAGAGATTCTT
TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTC
AAAGCGTCGATGCTCCAATTAATATCTCTCTCAGGGTGTAGTGCCTTCTTTGAAAATATAGATG
ATTACTTGAGACAGGAAAGAAGAGAAAACCTTTTGGGTACCATTAAAGGATCTCAGAGATGTGA

CTGAAAAGTATCTTGTGATAACCAAAACAACCTTGTCACTGTTATTGGTGACAATGAAATTTTAA
ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328)

MLKTRLKQSRASRVVRRYACSHPI SPNLDPVGLKLHGVEVTQTSP IPEFSLTAVSLKHTESGA
THLHLDSPNDSNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNMT
GHDYTFYPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE
MKGQYSNSAYFYIKFLESITYPSLNNSGGDPKKIVDLSYEGLLFHSKNYHPSNAKTFTYGLPLE
DSLKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCTSI TWNLGNP
LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNYLTKQK
VDNFNEKVMELINNKKIIPELSNEESSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIVPSWVNGV
DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTLCNPHSQKFKFTMEPREDFTKQLVKDENLMIE
KRVSELTEDNKKAIYEQNLELAKLQLEDQNTFVLP TLTIDDI PKRGDFY AIDLGQVNNKKVVHERVV
DTNGLVYANALKDISYLP TKLYKYLPLFNNCLTNLAGTENTPITELETKI QMLTGGITFSSKISTD
PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILTTTKFDTSDDEVLEKLSVLIKNMGQNNIINNIADR
GHSYAAAVSSSKLTPSKYISDIVSGLSQVQFVMELNSKLESEGKEYLAKEIIPILQEIQKYVLQGE
FRYRLVGNQEIIVENEKLIEKFDKDISSNRPTLSLTVT DGLSALLNSFNYNHTSENVLVNLPFQVG
YSSLGKIGSSSYSSKDGASLQILSQLYSFKNLHHSKIRESN GAYGGGLTYDGLNGTLNFYSYRDPNPV
KSIQTFRDSL SYGLDANWNDKDLQEA KLRVFSVDAPINISSQ GASAFFENIDDYLRQERRENFLG
TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNVDNKKWQIRNFQV

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548,
intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)

TAAAGAACTAGCAGATGTAAATGTTTTATGTCAATTATATAATTTGTTAATACATGTATATAGATT
TTTTAATGAATGTATCCCTAAATAGAACAGAATTATGATGCTGTACAGCAAAAACCTGGTTTGAG
TATTGGAGAATGTTATAAACTGAAATTTGATTTACAACCAAAACCCGTGTACGTGTAAGTAATTA
GGGCTTTTAGGGCTTTCTATATACAGGCACCAAGATTTTTTTTTATGGGCGATAGAAATAATGTAT
GCGCGCGATTCTTCCTGCTAGAGGTTTTCTTTTTGTATGTCTGTAACAGTGCGACTCACATAGTT
AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCTAATCACATAGTTAATTCTCAAA
CTTTCTCTCTCTCTCTCTTTGCTTTTCTCCTAAGGAAAAAAAATTTATTTCAATTTGTTGAAAAT
TTTTGTATAGTTTCAGTTTAAACAACACCAGTAATCAAACATGCCATTAGTTGTCCAAGAACAGGTT
CATTCCAACACATTTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGTT
AAGGAAGGAAAGAAATTATCCAACACTACTGTTTGGGAAAGATTAATCAGAAATTTGAATGCAATGA
AAAAACTTTTTCAAGAGATGGATATGGAACCAAGATTCGATTGTTATCAACAAATATAAGAAAGC
AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATACTACTATTTACTTTGG
AGTAATATGTTTTCAATATTATCAGAGACTTATCAAAATTTATGAGTTTATTATTATTGAAGTTCA
ATACCATCAAGCCTTTTTTTTAACCATCACTCTATTCAACAATCATTTAAATATTAAAGTCTTTTT
TTTCCCTGTTTAAAGTATTTCGATTACTAACAATTATGAATTATTATTATAGTTTGTAAACACCAA
CATTGATGGTAGAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC
CAACTTGGTTTGTAAAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGAATTGACCCAAGAAGA
ATTGGAAAGAATTGTCACCATATTGCAAAACCAACCAACTATAAAATCCCAGCTTGGTTCTTGAA
CAGACAAAAGATCAAGTTGATGGTAAAGATTACCATGTTTTAGCTAACAACCTTGAATCTAAATT
GAGAGATGATTTGGAAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT
GAAAGTTAGAGGTCAACATACTAAACTACTTCTCGTGGTCGTTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)

MPLVVQEQGSFQHILRLNTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKLRDDLERLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

YDR471W_YHR010W_homolog 1327bp PathoSeq: 1..1327; exon 1:

501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)
ATAGTTATTACAATATAATAAAGCAAATAAAATAAAAGAAATGATAAAGAACCATATTAACAAAGTT
TGAACGTGCTGTAAGTAAATCTTGTATACGAGAATATTCATCTTGGAATATTTCTAAACGATACTG
GTAATACCTAATTCTATTTGGTGTGGTGCATCACGTGCTAGGGCTATAGCCCTAATAGTATATGCA
GTCGCATACATTAATTGGTCATCTCATAAGTAAATTATATAATGTATAGTGTGCGCGCACTGTAAT

TTTTCACACTAAGTTAAGGAGAGTGCAGAAAAATTTAGTACTAACAAAAATTTGTATTGTGTTGTGTGT
GGCTATTGGGCAGAGCGAAAAATTTACCCCTACTGAGAGGAACTGTGAGGGAGAGAGATACACAC
AAACTCTGTGCGCAAGAAGAAAGACAAAAAATTTTTTTGAAAAAAAAAAAAAGAGACAACCAACCTT
TTATTGTATTAAACATTTTAAGATATCAAGAACTAAAAATGGCTAAGTTCATAAATCTGGTAAAG
TTGGTATGTAAAAATGAGTACCTATATGGGTAGACAATGATAGATTTATTGGCCAACTATGAATGG
GATAGATATATATGATATGGGAGAGAATTTTGAAGGATTGAAATATTTTATATAAAAAGAGAGAAGC
AAAGAGAAATAATGAACAATTGAAAAGAAGATACAAATACTGTTAATTAACTAGAATATGCCATT
GAAGATTTAAATGATTACCATCGTAATAAATTTATTGGAATTTGGGAGATTCTTTTGGAGTTAAGA
AAAAGCAAGTGATTGATCAATCACTATGGAGCCGTCACAAGACATCAACGAATCCACAAACATTT
TTATTTATTTCATATCCATCATATGGCAGTAACAATCATGAATCTACAAATTACATTTAAAAAAGC
ATTATACTAACTAAATTTTTTAGCTATTGTTGTAAGAGGTCGTTACGCTGGTAAAAAAGTAGTCAT
TGTGAAACCACATGATGAAGGTACCAAAATCTACCCATTCCACATGCCATTGTTGCTGGTATTGA
AAGAGCTCCATTGAAGGTTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAAGAACTAAAGTCAA
GCCATTTGTTAAATTAGTAACTACAACCATTTAATGCCAACTAGATACTCATTAGATGTTGAATC
ATTCAAATCTGCTGTCACTTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT
TGTCAGAAGGCTTTTGAAGAAAAACATCAAGCTGGTAAGAACAAATGGTTCTTCCAAAAATTACA
CTTTTAA

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332)

MAKFIKSGKVAIVVRGRYAGKKVIVKPHDEGTKSHFPFHAIVAGIERAPLKVTKKMDAKKVTKRT
KVKPFVKLVNYNHLMPTRYSLDVESFKSAVTSEALEEPSQREEAKKVVKKAFFEEKHQAGKNKWFFQ
KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

TTCCAGTCATTCCGAAATGCATAAGCAAGACGTTAGTTGTATTGTGGTTGTTTAGTCTAATCCAAA
AATACCTGCCATGACGACCCACTGAAGTAACAACCTGCATTTGTTAAGGCTTTTCTCATCTTATTCA
ATTCTTTTTTCAGCATCATTCGTATCTTTAAGCACAGGGAATAGCAATGGATCATGTAACAAATTCA
CTTTCGTGATTGCAAGGCCCAAAATGTTTCGTTTTTAACAACGCACACACATGTGAAACCTAAACCG
AGTTAGTCGTCAAGAAAATAATTCAGTGTTAAAGTCTGTACCTTAAGCGTCAAACGTACTTCTGCA
ACCTCTGGCATTGAGTGTAATTTAAATATTCATGATAATCTGGAACCTACAAAGCTACGAAAAAAAAA
GAAAAAGAAAAATAGTACGAGTCTTGGTGAGATAAATAATGGAGAACACTTTTTTTTTTCTCTTT
GGAGGTTTTAGAAAGGCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAAGCA
CTGCGCCCAAAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG
TTAAATTAAGCAAGATCAACTCGGAATTATCCACATACCAACAAAAGATAAGCAGAATGAGAGACG
GACCCGGAAGTCGGCACTAAAAACAAAAGCAATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG
CTCAAAGGATCAGTTAGAGAATCAATCTTGAATATGACACAAGCTTCCATGACAACAGATAACT
TACAAAATACCATGGTCACAATAAATGCAATGAAAACAGCCAATAAACTGTTGAAACAAACTTATG
GAAAAATTAATATCGATGAATTGGAAGATCTTCAAGATGAAATGTTGGATTGATTGATAAATCAA
ATGAACTACAGGAGGCACTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG
ATGCTGAATTAGAAGCTCTTGGCGAAGAAATTGATTTTGAAAATGAAATGGCAGAGAGTGGGATAG
GTGCACCTAGTTACTTAAATGATACAGAACCTACAGCAGCAGATAAAATGCCTACATTTATTGACG
AACCAACCAGAAGAAGCTCAAAAAATCGCAAACCTAG

YDR486C_homolog 218aa (SEQ ID NO 334)

MNRLFGTKSTAPKPSLNDAIKIDERVGS�DVKLSKINSELSTYQQKISRMRDGPGRSALKQKAIK
LLRQRKQIEAQKDQLENQSWNMTQASMTTNDLQNTMVTINAMKTANKSLKQTYGKINIDELEDLQD
EMLDLIDKSNELQEALSTSYDPDDISESELDAELEALGEEIDFENEMAESGIGAPSYLNDTEPTA
ADKLPTFIDEQPEEAQKIAN

YDR507C_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS: 501..4547 (SEQ ID NO 335)

GAATGAGATTTTTTTTTTTTACTAAGGGTGCCTACTACTAGTTATTTGTTTTGTTGTTGACGATCA
TTAAAGAAAAAATTTACAGTATACACAAAACACTTTACTTCTGCTGTTTTTTTTTTTATTTTAGTTT
TTGGTTTTCATAAATTATTTAAAGAAAGCAAATAATTATTGAAATAAATTTTATATTTTTTGGTTTTT
TTTCTTTTGGTTTTCTTTGAATTTTGCAAACCAATCCAAATTTTTTTTGAATTTTTCTTCTTCT

TCATTTGTTGACTTTTGAAGTTTTATTCATCCATATTCTTCAAGTTAAAAATAGTGTTCATATCT
GTCCAACCAAGAAGAAAACCAATAAACACATCAATTCCAACCTTGTTTACATCAAACAGAAACAA
AAAACAGATAATTTATAGACACCTTCATTCATTCGTTATTTTTTTTCCAAGTACTACACGTCTTTAT
TTTTAATACATTTTATCATAAACAAAATTTATATCAATAATGCCACATTCAAGACAACCTTCGATAT
CGTCATCGATTATGTCCCAATCAAATCATAATCATCCACAGAAGATCGGACCTTGGAAATTAGGTA
AAACTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATTAGCTACTCATCAAACCTACTGGTCAAAAAG
CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT
TACCATATGGTATAGAAAGAGAAAATTATTATAATGAAATTATTAACCTCATCCTAATGTTTTGAGAT
TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTTGTCTAGAAATACGTTGAAGGTGGAGAAT
TATTTGATTTATTGGTGGAACGTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAAA
TCATATTGGGTACGGCTTATTGTCTGCTCTTGGTATATGTACAGAGATTTAAAACAGAGAATT
TGTACTAGATTCTCAATTGAATGTAAAATTAGCCGATTTTGGAAATGGCAGCTTTAGAAAAGTAACG
GCAAATTATTAGAGACTTCTTGTGGTTCACCTCATTATGCTGCTCCAGAAATCGTTAGTGGATTGA
AATATCATGGAGCTGCTTCTGATGTTTGGTCTTGTGGGGTTATATTATTTGCCCTTGTGACAGGTA
GATTACCCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA
TGCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAATGTTAGAGGTTGATCCTA
TGAGAAGAATATCTACTGAAAAATCTTAAGACACCCATTGTTAACCAAAATACCCAATGTCAAACG
AAGATTTAATCAGTGAAAAATCATTACCACATCCACATACTGGTTACAAATCTTTAGGGTCAGTTA
GAAACATTGATAAACAGATTTTATCAAACCTTGACAATTTTATGGAATGATAGACCCGAAGAGGAAA
TTGTTGATTGTCCTTTTGAAGATGGATCCAATCCAGAAAAAACATTCTATGCATTTATTGATGAGAT
ACAAGCATAATCAAGACGATAACACTAATAACAATTCACCAAAGAAATCAACGAGTTTCAATAATA
AAGTGGTACGCAGTGGGTCCAAATACAGTCTTAATGGAACCCCTAGAAGAAAAAGAGCCAGTCACA
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GAACTCCGTTGCCAGACATTCTGTGGCTTCCCTCGGCCAACAATCTCCTCGTAAATCACCATACA
AGTCACCATAACAGATCACCTTATAGATCACCATATAAATCGCCTTCTAAGAGATATTATATAATC
AATCCCCAACTAAATCTCCTTACGGAAGAAGATCAAATTCACAAAGACAATTTGAAAATGAACCAT
TAAAGGCAAGCCAAAGAAATATTACAAATGAGATTGTTGATGCACAAAGCAACTTTTCTCTACCTC
CATCGCTTCCACCTTCCCTTACCTTCAAAAGATTCTCGTTATATGATCGATGAACCCAATCAACCCC
AGTTGCAACAACCTGCTTTAAGTCAAGTCCCTGAAAATCCTATTGTTGATGAATCCCCTGATTTAA
TGCAGTCAGCAAAAATTTCTAGTGGAAAGAGAAATTCATAATAGGAAAGAACAAACAACAGCA
ACAGCAACAAGAGAATGTCTAAGAGAAAATCAATTCGTGCATCTATGACCACGGGATTGAAAAGAA
ATTCATAACCATGAAATTGTTATCTACTTATGCTAAATTATCAGGTGATGACGACTGGGAATACA
TGGATAAACAACAAAAGAACATCGGCTACTTTTTCAGCATTGTGTGACAAAATTTAATCAAG
AAGAGTATGACGAAGAAGACGAACAAATGATGATTGTTGATGCACAAAGCAACTTTTCTATGAAA
GGTTAATGGAATTGGAAGAAAAGAAAACATGAAGCTGAGTTGAAAGCTAGAAGAGAATTAGAAAAGA
AGAAAAGAAGACAAAAGAGACGTTCATTTTGAATTCTAAGAAATTAAGTATTATTGTCAAGAATG
ATGCTGATCCAAATAATAGTGAACAAGAGTTGGTTCGATGAAGGTATAAAACAACCAAAACGTCAAT
CCAAAACCTTGACCGCTTTAAGAGCATTATCTGAAGGAAATCATGCATCTGAAGAATTGACATTGG
AAGACGTTGAGAATTGGAAGAGACGATCAGCATCACAGCCGGTTCCAAAAGAGACAAAACCTCCGG
TTTTGACAAGAAGACCTGTATCAAGATTAGATCCATTATGGCAAGCACACGAGAATTGAACAGTTAG
ATAGAGCAAAAGATGCCTTGGAAACAAGATGGAGGGATTACAAAAAGAGAAGTTCTACTGTTAGTC
GTAAAAAGTCAACAGAGAGTCGATGATATCAGTTATGGATGATATTGTTGAAGAGGACCAAGGCC
GTGTCAACAGGAGATCAACACGAAACACTTACTATGAAAGGGAAAGAGACTATGAATTACCAGAAC
CAACTGTGGAAGATTCCAACCTTGACTGATGACTACATGACAGAAATCAGAAAATCAAGACTTTTGA
ACAGTCAGTTAAATGTTAGGGATCCACTTAATGAAAAAGAAAATCTGAACCCAAGACTCTTATTA
GCAATGTTCAAATACCGAGTGTTACTAGAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT
CGGTATTGCTATGTATTCAACAAAGGAATCATACCGTGATTTGAATTCTATAATTAACCTACCAG
ATGAAAACCCCGAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAAGTATTGCTGATCGTT
TGGATAAAGCTGGATTGGCTGAACCAGAATATGAACTGAGACTGATGGTGAAGATAAAGTGTCTG
TTATTGATTTGGATGATCATTTAGCTGATAGAAGGACTTCTATTATGATGGATCTGGAAAGAGAG
CATCTAGAGCTTCAACAATAAAACGTTACAATGTTTCATTCCAGTTCAGAAAAAGACCAAAATCCA
AAGTTCCTGATTTGCCAAAGAATGATTATGATGACACATTTGTGAGTAATAGTGATGAAGTTCATA
AGCGTCAGTATAAATCGATGGTTTCTGATGAGTCTAGTGCATCTGATGATGATTTTGATAAGATTA
AATTACCAGATGGTAAATCAACTAAATCTTCCATTGATGAATTGGCTAACGGCACGCTCTACAAGTG
GTCATAGAAAAACCAAGATAAGACATTCTCAACCGGGCCAGAAATGTTGATTCCTCATTTGAATG
GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTTCGTGGTAACAATTCAAGTGGTCATGATGATA

GTGTTCCACCACCACCGCCAGCTCACAAGGTGAATAAAAAACCATTGGATGATAAGACGAATTTCC
CTCCACCAGAAGTGGATCCAAAAAGAAAAGGTTTCATTTTTTAGAAAACTTCTTGGGGATCCAAAA
AAACCATGAAAATAATACAAACGCCGCCACTAATACCACGACTCAACAACAATTACCAAGTCCTG
CTGAATCAAAAGAGGAGAAAACCAAAAAGTTCATTTTTTCAGATGGTTTTTCGTCATCTAATACTCCAT
CTGCTGCTGAAATTAGAAAATTCAACACCATTTTACCTAAACATGAAATGTCTACTGCTTTATTG
CTTTATTGAATCTTGGTCTAATTTTGGTTTGAAAGATTTACGGAATGATCAAGTTGGATATTATA
TTACTGGTGTCTATTTCTAAACATAATCTTTTAATTTAAAGAGTTGTAAATTTAGAATTAAGATTA
ATCAAAGAGATTTTAAATCAAAAATCAGAAATTGTTTGTGTTAGAGTGAAAGGATCTAAAGTTACAA
CTGATACTTTATTTTGTGAAATTGAAAAGGTCTTACTCAAAGAAGGTGGTTTAGATAAATAA

YDR507C_homolog 1349aa (SEQ ID NO 336)

MPHSRQPSISSSIMSQSNHNHPQKIGPWKLGKTLGRGATGRVLLATHQTTGQKAAVKVSKSELQD
EETEKNGDGLPYGIEREIIIMKLLTHPNVRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE
VEAIKYFRQIILGTAYCHALGICHRDLKPENLLDSQLNVKLADFGMAALESNGKILLETSCGSPHY
AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLLKVQAGNFEMPVDEVREARDL
IARMLEVDPMRRISTEKILRHPLLT KYPMSNEDLISEKSLPHPHGTGYKSLGSVRNIDKQILSNLTI
LWNRDPEEEIVDCLLDKGSNPEKTFYALLMRYKHNDQDNTNNNSPKKSTSFNNKVVRSGSKYSLNG
TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYRSPYK
SPSKRYSYNQSPKSPYGRRSNSQRFENEPLKAKPRNIYNEIVDAQSNFSLPSPSLPSKSDSR
YMIDEPNQPOLQOPALSQVPENPIVDESPDLMQSAKISSGKRNSIIGKNMNNNSNSNKRMSKRKSIR
ASMTTGLKRNSITMKLLSTYAKLSGDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP
EEKEAKEYERLMELERKKHEAELEKARRELEKKRRQKRRSILSSKKLSIIVKNDADPNNSEQELVD
EGIKQPKRQSKNLTALRALSEGNHASEELTLEDVENLKRRSASQVPVKRRQTPVLTRRPVSRLDPL
WQAHENEQLDRAKDALEQEWDRDSQKRSSTVSRKKVNRESMISVMDDIVEEDQGRVNRSTRNTYYE
RERDYELPEPTVEDSNLTDYMTETIRKSRLNSQLNVRDPLNEKRKSEPKTLISNVQIPSVTRKSR
NFTTSNKRLSVLSMYSTKESYRDLNSIINSPDENPEQHQNMMNKPALRTSIADRLDKAGLAEPEYET
ETDGEDKVSVIDLDDHLADRRTSYDGSGRASRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT
FVSNSDEVHQRQYKSMVSESSASDDVDFDIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG
PEMLIPLHNGGIESSQPMKVRGNSSGHDDSVPPPPPAHKVNKKPLDDKTNFPPEVDPKRKGFS
FRKLSWGSKKTIENNTNAATNTTTQQLPSPAESKEEKPKSSFFRWFSSSNTPSAAEIRKFNTILP
KHEMSTALFALLNSWSNFGKDLRNDQVGYITGAISKHNSFNLKSKFKRIKINQRDFNQKSEIVC
VRVKGSKVTTDTLFCIEIEKVLLKEGGLDK

YER102W_YBL072W_homolog 1121bp public: 1..1121; CDS: 501..1118
(SEQ ID NO 337)

ACAATACTAGGCACTGTTGAGTGAGTGAGCATTTTTTCTGTTTCTCACTCAGTTAACAAAATAAAA
AAAATTTTCATAATTTAGAAAGTTTCATTTACAGTCTTTTTTCAATTAACAGTGATACAAGAGTGTA
TGTAAGACAACATGTACTAGCAACTATAATATGATTTACCAATGATTGGGATCACAATAAATGTG
TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA
TGGTATACAACATAAAATGGAATTATTTTCAAATATGCAACTATCATTATGACTACTACGACAACAA
TTTTAATCGAGAGAAGATCATTAGATCAAGAGTTGGGAAACTAATAACCAAGGAAATATCATTAAGA
ATTAATAGCTTTGCAAAAATTGGTTTTACTCATATTATTTGTTTTAGTTGGAAAGCGATTACATCA
TGGAACAAAGTTTACTAACAACATTGTTATAGGTAAAAATGGGTATTTCTAGAGATTACAGTCACA
AAAGATCCGCCACTGGTGCCAAAAGAGCCCAATTCAGAAAGAAGAGAAAGTTTGAATTAGGTAGAC
AACCAGCCAACACCAAGATTGGTCCAAAAAGAATTCACTCTGTGCAAGCAGAGGTGGTAACCAAA
AATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTCTCTTGGGGTCCGAAGGTGTTTCCAGAAAAA
CCAGAATTGCTGGTGTCTGTTTACCATCCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA
AATCTGCTGTTGTTCAAATTGATGCTACTCCATTACAGACAATGGTACGAAACCACACCGTGCTA
CTTTAGGTAAAAAGAAGGGTGGTGCTCATGCTGCTCACGCTGCTGAAGTTGCCGATGCCAAGAGAT
CAAGAAAAGTCGAAAGAAAATTGGCTGCTAGATCTGGTGCTGCTGCCATTGAATCCGCTGTTGACT
CTCAATTCGGTCTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGATGTG
ATGGTTACATCTTGGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAATAA

YER102W_YBL072W_homolog 206aa (SEQ ID NO 338)

MGISRDSRHKRSATGAKRAQFRKKRFELGRQPANTKIGPKRIHSVRTRGNGKFRALRVETGNFS
WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTKSAVVQIDATPFRQWYENHYGATLGKKKGGAAHAAH

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY
LRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTGTG
TACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTCCA
AATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTGCTATCGATAACGAAGG
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAAAT
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACACCACAGCAATATAGCAA
TCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCCTTGAATCTTGTTTTTT
TCGACATACACCATAAATCCCATAGAAAACGCAAAATGTCTGACGCCGGAAGAAAAAACATTTCT
ACTAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAACAA
GTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAATCTTTCCTCAA
ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA
CAAGCAGAGGGCGAAACAAAGACCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAACG
AAATTGGAAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADSVQQGSDN
AKADLKKQSEQAEGEQRLSKQLKNMSRLPKSKLERSNST

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTG
TGTACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGT
CAAATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTGCTATCGATAACGAA
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACACCACAGCAATATAGC
AATCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCT
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCCTTGAATCTTGTTTTT
TTTCGACAAACACCATAAATCCCATAGAAAACGCAAAATGTCTGACGCCGGAAGAAAAAACATTT
CTACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAAC
AAGTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAATCTTTCCTC
AACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG
AACAAGCAGAGGGCGAAGCAAAGACCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAA
CTGAAATTGGAAAGGCTGCTGAATACGTGAGTGGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA
CCGGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADNVQQGSDN
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTAT
TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTCTTCGAGTCTTGGTATCGGTTGTAAACG
TATCTGTTTCACTTATCAGTATCGTCATTTATATTAATACTACTTTTCTCCTATGGTTATATATTGGT
AAACAAAGAAACAAACAAACAAAAAGAAGTAGTATTTGAAAATGTCAATAAAAGAAACAAAG
AATGAAAGAATGATTGAATGAAAGAAAAAATATGAAAGTGAGTGCAGACATAATGTAGAAAAA
TGTCGAATGTCTTGAACCTTACCCATTGAGTAGTTGTTGTAGTGTAGGAGGAAGAAACAACAGAA
AGAAAGAGAGAAAGAAAAATTTCCGCACTACAAATATTCAACAAGTTTCATATAGTAATATAATCC
CAATTGATCATTACTTTATTCACACAATTTCATAAACAATGTCCAATTCAGCAGGTTTTGATAGAC
ATATCACTATTTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT
CAGCAAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATCACAAAAGAAGA

TCCCAGATAAGTTATTAGATCCTAAAACCGTGTCATATATTTTTTAAAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAGTTTATCAAGAAGAATGGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTGGGTGTTGCTTTAACTTTTATTCAAGTTG
ATTTTGCTGATGAAGGTAGAGGTCCACAAATTTTTTAAATGTGATCCTGCTGGATATTTTACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCTG
TGATTGGAAGTGAATTCAGAAAAATGATATTGAAATTGGTGTGGCCACTGAAGGAGAATTTAGAA
TTTTGACACCAGAAGAAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

YGL011C_homolog 247aa (SEQ ID NO 344)

MSNSAGFDRHITIFSPGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRARSEATEFRYKYGVEPESLSRRMANISQLYTQRAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQOEATTYLEKKFKKTDVKGDWQKTV
EFAIIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

CATTGTAGGTACACCTGTTTTTGTCTCAATGTACACACACACGCACCAGCAGTAGGAAAAAACA
AATTAAATGAAAAATCATTTTCGTTCAATATTAAGCTTCTTAAGATAACCAACCAATTAATATGTA
TGTGACATACCATATAAATAAAGCTACAAATGGGGATAACTATGTATTTAATGATAAATGAATGGA
AGACCAGAATGTATAATGTTATAAGATAGTGATTTATATTGAAAACACCCTTAAAAAATCAACCA
CCCATCTAACCGTCGAATTGGAAATGTCAATTTAGTTAGCATCGAAAATCAACAAAGACATGGGGA
ATCATTTACATATAAAATAATGAGAGAGAATTACAACTGCTACGTTATGTTTTGTTTCATTATGTC
TTGTTTCATTATGTCTTGTTCATTATGTCAAAAAATCTATAGTTACCTACCTCTACATCAATTTATG
GTCTGAAATACTAACATTTTTTTTATTTATAGTGAAAAATGAAGATTGAAGTTGACTCCTTTTCAG
GTTCTAAAATCTACCCAGGTAGAGGTACTTTATTTGTCTAGAGGTGACTCTAAAATTTTTTAGATTCC
AATCCTCAAAATCTGCTTCTTTATTTCCAACAAAGAAAGAACCAAGAAGAATTTCTTGGAAGTTT
TGTACAGAAGACACCACAAAAAAGGTATTTCTGAAGAAGCTGCTAAAAAGAGAACCAGAAAGACCG
TCAAGCACCAAGAGCTATTGTCCGGTGCTTCTTTGGAATTGATCAAGAAAGAAGAAGTCAAAAAAC
CATCTGACAGAAAAGCTGCTAGAGACTCTAAATTAGCTAAAGACAAAGAAGCTAAAAAAGCTGCTA
AAGCTGCCAGAAAAGCTGAAAAGGCTAAGGCTGTTGCTTCTGGTGCTTCTGTTGTTTCTAAACAAC
AAGCTAAAGGTTCTTTCCAAAAAGTTAAAGCTACCTCCCGTTAA

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346)

MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE
AAKKRTRKTVKHQRAIVGASLELIKERRSQPKPSDRKAARDSKLAKDKEAKKAARKAEKAKAVA
SGASVVSQKQAKGSFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

AATCTACCATTAGGCAATGTCATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT
CCATAATTTATAATGGCATACCTTTGGATTTACCTGTTAATTCATCAAATAATAACTTCACATCT
AATACTGGTCCAACGTATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA
CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCCTGATTCTT
GGTAACAAAAAATATAATTATTTAACAAATTTATCGATAGAATCTCTTCCAAAGTACAACCAATTT
CGATACATTTTTTTCTATGAGATGTTTTTTTCCCCTTTGTCTTTAACTAATGTATTTGGGTACACT
ACCTGAACCTACCAGTTTCAGTTTCAGTCTAAAAAATTTTTTATTTATTGTTGTTTATACTACCC
TTTGCATATATTACTAATATTTATCTTACCCTTTTCATCATGGATACAAAAGGAAATAAGATCTACCG
TATCTAATCTTGAAAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG
GGGTAAACCATCCGAAAACTCTTGAGAGAAACCAAAGTAGGTGTAGCTGTCAACAAATTCAGAA
GTCACGACAGTGCCGAAATCAACGGTTTAGTTAAAAAATGATCAGAAATTTGGAGAGATGCCGTGC
AAGCCGAAAAGAACAAAAAGAGTTAGCAATAGCAGCTGGAACAGGAACAGGAACACCTTCAA
GCTCAGCAATTTGCGCATCATCATCGGGTTCTGGAAGTACAACACCAAAACCATCAGAGTCAACCA
CACCATCGGCTGCCCGTAAAGGTCCAAGAAATCCAAAACTGACGGTGTAATACTCAATTATACG
AAAATGATACCAGAAATGCATCGGTTAGTGCTTTTATACACGTCGTTAGCAGTTGATCGTGACGATT

CACCAAAACACATTTTGAGAAATAGCTATTGAAATCGAGGCTGAAGTATACAAGAGCGAATACCTGA
AAGTAAGTGACAGTTATAGAAATAGGTTAAGAAGCTTTACCATGAATCTTCGAAATAAGAAAAACC
CAGAATTAAGAGAAAGAATCTTATCGAAACAAATTTTACCTGCTGCGTTCATTAAAATGACCCCTA
ATGAAATGGCTCCTGAGGCATTGAAAAAGGAAATTGAAAAATTGCACAAACAAAACCTGTTTGATG
CTCAAGGTGCTACTGAAAAGAGAGCAGTGACCGATAGATTCACTTGTGGCAAGTGTAAGCACAGA
AGGTCAGTTATTATCAAATGCAAACCAGATCAGCGGATGAGCCTTTAACTACATTTTGTACTTGTG
AAAATTGTGGCAATAGATGGAAGTTTTCATAA

YGL043W_homolog 305aa (SEQ ID NO 348)

MDTKEIRSTVSNLEKAVDDTTILKLLNLDGVKPKSEKLLRETKVGVAVNKFRRSHDSAEINGLVKK
MIRNWRDAVQAEKNNKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTSIAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNRLRSF
TMNLRNKKNPRLRERILSKQILPAAFIKMTPNEMAPEALKKEIEKLHKQNLFDAQGATEKRAVTDR
FTCGKCKHKVSYQMQTRSADEPLTTFCTCENCGNRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon
1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)

ACATTTATTGTTGGCTATACTTTCCAGTTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT
TTTACTGTAATGTGTTGTGCCAGTGTAATGTTTATCAAGACTAAAGTTCCCTGAGACAAAGGGTAAG
CATTCGTACCAGGAAGTCTGGAATTAAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT
TTGTGCTCTAAAGTTGCGTTAGGGCTAAAGCCCTAATCAATAGTAGTGTACTTTGTTTGAAGAAAAAT
AATACATGCAAATACTGCATATTAGAATTATAAGGGAATGAAATGAAAAAAGAAATAATTT
TGTAAGATCGCATAGTGTGAGCGCGCACACACACAACTTTGTAGTGCTACAGTTTCTCTCTTTC
CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCCTT
TTGAGTTTTCCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAACATAAACAGAA
AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTAAACGGATGAAAGAGTATTGA
ATGTTCAAGGACATATGGAGATTTAGAGAAAACATGGAATAATCGAAAAATGAATAATGAATGG
AAAATTTTTTAACTGAATATCAGAATAGACACAACACAGATCCAGAGTCATTATCACATTGA
TCATACAACCAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTTTCAGAA
CAATCAAGTTTATCATTTACAGAAGACAGTTCCATCAATATGTCCAAAATCTCTTTGAAGTCAAT
TAAAGTCAAATGAACGAATTACTAACTTATTTTTTTCTTTAGCCGGTAAGGGTAGAATTGGTAAAC
ACAGAAAGCACCCGGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCAACTTGGATA
AATACCATCCAGGTTACTTCCGTTAAAGTTGGTATGAGATACTTCCACAAACAACAAACCACTTCT
GGAGACCAGAAATCAACTTGGACAAAATGTGGACTTTGGTTGATTCTGAAAAGAAAGACGAATACT
TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT
TGGGTAAAGGTAGATTACCAGAAGTCCAGTCATTGTCAAAGCCAGATTTGTTTCTAAATTAGCTG
AAGAAAAAATCAGAGCTGTTGGTGGTGTGTCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)

MPTRLTKRKHGRNVSAAGKGRIGKHKHPGGRGKAGGQHHHRTNLDKYHPGYFGKVGMRYPFHKQON
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLEVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO
351)

GCTATCAAAATCACTGTTTCAATGGTGACAGAAAACACGTTGCTGCTTTAAGAACTGTCAAATCT
TTGATTGCTAACTTGATCACTGGTGCTACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCG
CATTTCCCAATTAACGTTAACATTATTAAGGATGGTCAAGATTACGTTGAAATTAGAAATTTTC
TTGGGTGAAAAAGAGTTAGAGAAGTTAAATCCATGAAGGTGTACCATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACTCCTTGAAGCTGTTTCTCAAAATGCTGCTGATATT
CAACAAATCTGTCGTGTGAGAAACAAGGATATCCGTAAATCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTTGTTGAAGAAATCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)

AIKITVHNGDRKHVAALRTVKS LIANLITGVTKGYKYKMR FVYAHFPINVNIIKKDGDYVEIRNF
LGEKRVREVKIHEGVTMEISSTQKDELIVSGNSLEAVSQNAADIQQICRVNRNKDIRKFLDGIYVSE
RG TIVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353)

GATGATCGCTAACAAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC
AACCTTAAATAGCTTGTAGTTTTTATGATTGGGACTAATTGTGCAGCATCGAACAATATTGCCAGT
TGCATAGAATAAATCGGTATTATTACGGCATACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA
TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTGCTGTGTAATTTGGTGAAT
GAATTGATCAGATGATCCTATGGGTGGCATTTGTTAAGGTTGTTTCGCTACGATGTATTTCTAGGATA
ATGAAGGTAAGTACGAACCTTATGAGTTTTGATTTCTTCTGATGTTTTTTTTTCTTGTCTT
TTGTCGTTGTAGCAAGAAGAAAAAAAAAAGTGTCTTCACAAGCTTGGACTCAATTTTACCCTT
CCACAACTCAATTTCAATTAACCTATCAATAATCCAATATGGGTAAACAGTATATATCTACCGTCA
GTGCATCTCAGGCTCATAAGCTGGATATCTTGGTGTAGCTATTACCAATAAGTTCACTGTATCCG
TGTCTAGTGATGGATATGCGAAATTTTGGGACAAACAAGCAAGACGAAGTTCACTGTCTTAAAGAAT
TTGTCCAACCTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGGCTGCTTACGAAAATGTTTTGC
CAAGCTCTACATTGAAAGTGACATTATTAGCATTTGCATGTTTCAATGGATCTATCATCTTCAGAT
ATTATATCAATGATGACTTTTCAACTATCGAAAGTCTAACTGATGATATAAAATCAATTTGGAAGCA
ATTGTTGGACCCCTGGCTTTTATCGCGATCCAGAATCCAAACAAGACTATTTTATTACAACCAAGA
CCAATGGCACTACAGAGGTTCAATTTATGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT
TTGAAAAGTTTGGGCAATTAAGGAACTCTTCTTCTTCCCAAATCTTTGGCTATATGTCCAA
CAGAGAATAAAAAATGTGCTGTGGGGTACATCAATGGTGATGTCTTGTTATATGACTTTGTTAGCT
TGAAATTGATATACACATTTCTGTCGAGTGATTTGGTGACCAGTAGAAATCCCAATCGACGTCTA
TACCTAGGGTGTTGGCATTTCCTTGGTGGAACCTTGTGGCTGTGGCAAGAGACAATCAAGCTG
CTGGGTCAATTACATTATACGACGTTGAGCATGGTGAGAATGTGGGGTCTTTGGCCACACCCTCAC
ACTCGGCCAAATCTGTTGTTGGTGGGTTTGCACATCAAGGCTGGATTTTGGGGTTGAGTTTGTATG
AGGAAGGTAAGCACTTGGCTAGTTGTGGATTTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA
GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG
ACGAGAGTGTCGCTTCTGGTGTGCTTTTATTAAAAAGGGGGTTAGAGGTGGCTCTGGTGGTGACA
GCAATGAAGGATTATGTGTCTGTAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA
TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFVSVSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH
AVAAYENVLPSSTLKVTL LAFACFN GSIIFRYIINDDFSTIESLTDDIKSFESNCWTPGFYRDPES
KQDYFITTKTNGTTTEVHLNLNIVDENEKAVITFEKFGQLKGNSSSF PNSLAICPTENKKCAVG YING
DVLLYDFVSLKLIYTFRSSDLVTSRNSQSTSIPRVLA FSPGGTLLAVARDNQAAGSITLYDVEHGE
NVGSLATP SHSAKSVVGGFAHQWILGLSFDEEGKHLASCGFDK CIRVWNLET SEREATISISISD
LDDTTHNDQDESVASGVAFIKKGVRRGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503,
intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATTCTGGTGGTTCAGTTAATTTATATCATGTCACTGAACAAGGTTGGACTTATC
ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTTGTAAATG
TAGATGGATAAAGTAAGTTGATTGTATAAAAAAGAATGGATTCATTAATATAAATTTACAAATCT
GATAATAAACTACAGTAACCTATTATGCAACAATTGAAAGTATCCTGTGTCACGTGATTAGGGCTCA
AAAGCCCTAACAGGTTGCACGTGATGTTGATTTATTTATCCCTGCACACATTGAGTTTTTTTTCTA
TGGTGAAAATTATTAGTGAGACGATGTTGTTTCGCATTTTACCACACACTCTCACACTGAGTGTAGT
CATACTAACAATCTTCTCACACTATACACAAAAAAATCTTTCGTTTGAAAAGTTTTGAAAGGTTTC
GTTTTCTCAATAGTATATCCATACATAAAGTCCAAAGATGGTATGTTCAGTGTTTAAAGAGATC
GAAATGTTTGTGTTTAAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG
AATTAATTGAAAGAGTTTTCTTTGGGGAAATGGGTTCAATAAGATTTTTCAAGATTGGAATCAAAA
TTATGTCAGATGTGAAGAAGAGTAAATATAACAAGAAGTTCAAATCATTAATAATTTATGTTAAAT
ACAACGATTATCAATTACAGTCAACGAATAGAATAAAACAAAAGCCAGCATATAACAGATACCAAGT
GATTCATCCCAGTGATATAAATAATGATATTCAATTAATAACAATATTAAGACATTTTTTATTAT

GTATCAACAAAATACTAACTTATCTTTCTTTTAAATTAGTCTGACAAATCCCAAAATGTTATGCGTG
AATTACGTATTGAAAAATTAGTTTAAACATTTGTGTTGGTGAATCCGGTGATAGATTAAACCAGAG
CCGCCAAAGTTTTAGAACAAATTATCTGGTCAAACCCAGTTCAATCTAAAGCTAGATACACTGTCA
GAACTTTCGGTATTAGAAGAAATGAAAAAATTGCCGTCCACGTTACTGTCAGAGGTCCAAAAGCTG
AAGAAATCTTGAAAGAGGTTTGAAGTTAAAGAATATCAATTAAGATCTAAAAACTTCTCTGCTA
CCGGTAACTTTGGTTTCGGTATTGATGAACATATTGATTTAGGTATCAAATATGATCCATCTATTG
GTATTTACGGTATGGATTTCTACGTTGTTATGGGTAGAGCCGGTGCTAGAGTCAACCAGAAGAAAGA
GAGCTAGATCCACTATTGGTAACTCTCACAAAACCAACAAAGAAGATACCATCCAATGGTTCAAGA
CCAGATACGATGCTGAAGTTTGGATAAATAA

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)

MSDKSQNMRELRIEKLVLNICVGESGDRLTRAAKVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKEEILERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGIKYDPSIGIYGMDFYVVMG
RAGARVTRRRKRSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTTGTGTGTATATGCGAGAAATG
AGTAATTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAATAAAATAAATGTCATATTGACAT
GATAAGGATTTATCAATACTGTTAGGTCATAGCCCTAACTTTAATCATTTACACGTGATACAAAA
AAGTTGTTTGATCCCGCAGACTATGAGTACGCACTCACTAATTATAGCCTGAAAAAAAATTTTC
CACATAGTAAGGGGATTTTGTATGGTGGTGCCTCGCCTAAGACGCTGCATACATTTTCTAAAGT
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTTCCCAACAAATAACTTTGCGGACACTCT
CATATACTCAATTTTTTTCTTACAAAAATTTTTTTCTTCTACTTTTTTCAAGAATTCTTCTTTTA
CAATTCACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAACCTCTGCTAGAAAATTAAG
AGTTCACAGAAGAAACAACAGATGGGCTGATCAAGCTTATAAAGCTAGATTATTAGGTACCGCTTT
CAAATCTTCTCCATTTGGTGGTTCATCTCACGCCAAAGGTATCGTTTTGGAAAAAATTGGTATTGA
ATCTAAACAACCAAACTCTGCTATCAGAAAATGTGTCAGAGTCCAATTAATCAAAAACGGTAAGAA
AGTCACTGCTTTTCGTTCCAAACGATGGTTGTTTGAACTTTGTGACGAAAATGACGAAGTCTTGTT
GGCTGGTTTCGGTAGAAGAGGTAAAGCTAAGGGGGATATTCCAGGGGGTAGATTCAAGGTTGTTAA
AGTTTCCGGTGTCTCTTTATTAGCTTTATGGAAAGAAAAGAAAAGCAAGATCATAG

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)

MKGKPRGLNSARKLRVHRRNNRWADQAYKARLLGTAFKSSPFGGSSHAKGIVLEKIGIESKQPNS
AIRKCVRVQLIKNGKKVTAFFVNDGCLNFVDENDEVLLAGFGRRGKAKGDI PGVRFKVVKVSQVSL
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

AATTCATTTGATCTCTAAGAAGATGAACAGGCCTTGAATGGGAGGGGTTGGTTGCACTTCCACGAA
ATGTGGTTGGAAAACTTGAGTCCTCAAAAAGGTTCTCTCGTAAAAGGCCAGAGAAAAGAAAAACC
ACCAAACCCCCACCAACCTAACCTTTTCCTTCCATCCATTCTCTTTCCTTACTTTGCAAATG
TTGAATCCAGTTATATTCAATTAAAGATCCTATAAAATACGATTATTCACAATTTATTATATCTTTA
CTCCCGAAATTCATTAATTGTAATCGTATTGATTTAGTTATACTTTGTCAAATCACCGAATCAAAT
CAATTGAATGAAATTTATGTTTTATTATCAATTAATTCGTAATCATAAGAATAATGGAGATACT
GATGGAGATACCGACAGTTTGCCATGTTTGATTATCGATTGAAATTAATATATTATTTAATTTA
TCAACAAAAAATGAATCAATTATGTTTAAATAAATTGGAATCATGGATATATTGCCGAAGGTGAT
AATGATAACAGTACTAACTTGTCACTTTGCCATTGTCAATAACAATAATCAAACATTGAAATT
CCAACAATCCAATCAAGAGCAAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAAATTACTACT
AGTCGGCAATATCAACAATTTAAACTACTGCTGTAGGTGGAACATTGATCATTTTACATGATGGT
CATAAAATTTTATTATCAATGGCAATTTTTTTAACTTCAAATAAATTAATTTATGGGTATAACTGGT
TCTAATTTATTAAATTAATAAAAAATTTAAATCTCAATTACAACTTTTAATCAAAGACAAAATTTA
GTTATTCAATTCATAAATTTATTATTATGAGTGAAACCAGTGTTATTTTTTTGAAATTTATGAA
ATTAAATGATGTTTGTGGTCCAACCTGGTTATATTAAATGATATTGATAATTAAATAATCTCAAGAA
ACTAAATCTGGTGGTGAATTTGTTAACAAATTTTCGTAAAGATCATGGATTTAAATTTATTAGATATT
ACAATAATTAAAGTGATTGGTGGGAATATTGAAGAAAATTCATGGAAAGGTAAATTAAGTTCAA

CTGATATTAGAGACAAGAATATAATCGATTATTAAATCAATAA

YGR277C_homolog 322aa (SEQ ID NO 360)

MLNPVFIKDPKDYDSQFIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD
TDGDTDSLPMFDYRFEINILFNLSTKKLNQLCLNNWNHGYIAEGDNDNSTNLSSLPLSITQISNIE
IPTIQSRANSSSAYNDEDDKITTSRQYQQFKTTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT
GSNLLINKKFKSQLQTFNQRLVIQFINLLLLSETSVIFFEIEINDVCGPTGYINDIDNLIISQ
ETKSGGEFVNKFRKDHGFKLLDITIIKVIIGNIEENSWKGLSSTDIREQEYNRLNQ

YGR284C_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAAATCTAAATCGTTCCAATGATTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT
TGGTGGCAGTAGTATTGGTATTAAGTGGGTGGGTGCTGATTGACTGCTGTTCACTTTATTGTTT
CGTTTCGTTTTTCTTTGTTTGTGACGTTGACATTTTTTTGCTGTTGTTGTTGTATGGGAATT
TTGTATTAGTTGTTCTTTTTTGTTTTTTTTACTTGTTCAAAAGTTTCATATAATAATAATATTCT
TGTTTTTCATATTTTTTTTTTTCAGAACAAGAACAATAACAACCTATATAATTTGATCTTACTCTTAT
CCCCAGGTTTTTCTATTTGTTTGGGTTTGGCATTATATATATATATATCTATTATTCAAATCAAT
TTGAGGAGTATCATTAATTTAAATTATATCAGTTAACAATGTCGTATCGTGGTCTAATCAATTTG
GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCACATATTGGTCCAATATCTTCCA
GCAAAAGTCCTTTAGAACAATTTGAAGATGTTGCTAAAAAAGTTGAAGATTGGATCGATGATTATT
TTAAAGTCTTGAAACCATACGTCCCAGCAATTGGTAGAGCATTTTTGGTGGCCACTTCTATGAGG
ATACTTTAAGAATCTTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACATAGACACTATT
GGCGTTGGTTGACCGTTTTATTCTTGATCAATAATATGGTGGTTATGACAGTTGCATCCACTTTAG
TAATTGCCAGAAAAAAGAATAACATTGCTACTATTGCATTGATCGTTGTTGTTATTATACAAGGTA
TTGGGTATGGTTTATTGTTTGATGCTCAATTTGTTTTGAGAACTTGTCGGTTGTTGGAGGGTTAG
TATTAGCATTTTCCGATAGTATTGTTAGAGATAAAAGATCCTTAAACATGCCAGGTTTACCGATGT
TGAACAATCAAGACAACAAAAAGTATTTCTTTTAGCTGGTAGAATTTTGTAGTATTATTATTTT
TGGGATTCGTCTTTCTCTGATTGGTCATTGGGTAGAGTTTTCATTATTATAATCGGGTTAACTT
CTTGTGCTTCAATTGTTGTTGGTTACAAGACAAAGTTTTTCAGCTGCTATCATGCTTATTGTTTTAT
TCTTATACAATGTGTTCACTAACCAATTCTGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT
TGAGATGAATTCTTCCAAGTTTGTCAATTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG
CTGGTGAATTCTCCATCGATGAAAAGAAAAAGATTTATTAA

YGR284C_homolog 308aa (SEQ ID NO 362)

MSYRGPNQFGNQPPHHGIPSQPQPHIGPISSSKSPLEQFEDVAKKVEDWIDDYFKVLKPYVPAIGR
AFLVATFYEDTLRIFTQWNEQVYLYHNRYRWRWLTVLFLINNMVMTVASTLVIARKKNNIATIA
LIVVVIQIGIGYGLLFDAQFVLRNLSVVGGLVLAFSDSIVRDKRSLNMPGLPMLNNQDNKKYFLLA
GRILLVLLFLGFVFSDSLGRVFIIIIGLTSCASIVVGKTKFSAAIMLIVLFLYNVFTNQFWAY
ASQDARRDFLRYEFFQVLSIVGGLLLLVNAGAGEFSIDEXKKIY

YGR285C_homolog 1876bp PathoSeq: 1..1215, public: 1216..1876; CDS: 501..1781 (SEQ ID NO 363)

AATTATTAGTTGAAAAACAAATCATACCTATTGCCAGAGCTCAAATGAAAGTGAGAATTACGTTAT
CTAAAAAAGCATACTTAAAGACTTTTCAAGATGAAATAAAACCTGTTATTGATCAAATTGTGGAGG
AAGATAACAATGGGAAACAATATGAGATTGTTGGGATTATAGATCCTATAAATTATAGAGTCTTGG
TCACATTAATTGAAAATACAGATGGAAGCAACAAGTCGCTAAAGGAGAAGGGTCTATAGAAGTAT
TAGATATGTCTGCCATAAAAGAATAAACTAACTAGACAAGTGTATAGAATCTTTTTTATTAAATA
GATGCTTATCTTAGTTATGTTCCAGAACAATTCATGTTAGGAGAGAGAGAAACGCAATCACTCAAT
TTTTGCACAAACAAAAACGAGAAGATGAAGAAGCAAAAAAGAAAATTTTTTTTCTCAACCATCT
TAAATCCTCCTACAATTAATTTCAATACCAATAAAGAACATGTCTATTGTATTACCATCAGGAACCTA
CTGACGGATTTAAAGCCGTCTCCAAATACTCTGCCCCAGTGGTGGTCCCAATTGAACCAGTTGGTC
GTTACTTCTTAGCCACGCCTCAAGAACTTTCGCTGGACACACTTGGTCTGAATTTGAAAAATTTGG
AAGCTGAAAAGAAATGTTAAACAATCGAAGTCAACGAGATGAGGATTGGGAGATGAAGAACA
GTGAAGAGTTATTAGAACACGATCCAAGAGAATGGAAGACTGCCAATTTATATGCTGTTTTAGGTT
TATCTCATTTGAGAAGTAAAGCCACTGAAGATCAAATCAGAAGAGCCACAGAAAACAAGTTTTGA

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAACGATGGATTTTTTCAAATTTATTC
AAAAAGCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTTCTATTGATGTTGAAA
ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG
AAAGTGAAGCAAGATTTTCTACTAAACAACCAGTTCCATTGTTGGGAAATTTAGAAAAGCACCAAAAG
AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGGAAGACTTTTGAATTCAAAG
ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAACGTTATATTGAACGTAAGAATATTG
CCCAACAGAAAGAAATTGAAGCAAGAGATCACAAGAGATTATCGAATTGGTCGAAAGAGCTCATG
CTGAAGATCCAAGAATTAAATTGTTCAAAGAAAAAGCCAAGAAAGAAAAAGGCTGCTAAGAAATGGG
AAAAAGAATCTGGATCAAGAAAAAGCTGCTGAAGAGGCTGCTGCCAAAAAGGCTGCTGAAGAGGCCG
CTGCTAAGAAAGCCGCCGAAGAAGCCGCCGCTTTTGAAGCCAACCTCAAAAAAGCTAAAGAAGCTG
CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG
GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGTCGATTTGTTAATCGAAAAATTCGACGATG
TCAAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAGTGAAATCTACTTTTG
TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCCTATTTGAAATATTTTAACT
AGATTTTTTTTTTTGTAGGAAAAATAATATATATAGAATGTAACTATCAAAAACAATTATACAGAAG
CTGAACCTCAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)

MSIVLPSGTTDGFKAISKYSAPVRRPIEPVGRYFLAHASRTLRLGHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHPREWKTANLYAVLGLSHLRKATEDQIRRAHRKQVLKHHDPKKSASGGL
ENDGFEKIIQKAFEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFEAWGPVFESEARFSTKQVPV
LLGNLESTKEEVDAFYFSWGRFDWKTPEFKDEDVDDTANRDHKRYIERKNIAQQKEIEARRSQE
IIELVERAHAEDPRIKLFKEKAKKEKAACKWEKESGSRKAAEEAAKKAEEAAAKKAAEEAAALK
ANSKKAKEAAKAAKKKNKRNIIRAAVKDNNYFGDSAKSADIDADVLLIEKFDDVKLGEVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLKYN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq:

538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175
(SEQ ID NO 365)

TTTCATTTGTAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAATATATATCCAAATAAGTC
ACATCTCAAATTTGGTAGTAGAAGAAATCAACCTTGGGACAGTATTCTCTGCTTAAATGAGTTTAC
TGATCAAATAAAATATTGGCTCAACCATTTGAAAAGCTATTCTTGACACTTTTTCAGTTTGTAGTTT
TGGTTGTTTCACAATTGAAAAAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT
ATTGCTTTGAGTGAAAAGTGACATTTGTACACACACAAAAAATACTAACCTTCTTCCCCCA
ATATGCTGCGTATAGTGAGAAATCTTCTCTCTCTTGGCCATACTATCGCATTTTTTTTTTTTGGTAA
CTCACGAAACCTAATTGGAAAGAGAAAAAGAGAAAAAATAATTTTCAGTTTTCATAGATTTTC
AGTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTTCATTAGATTTTACCATGAG
TTATGGAGGGATATTCTTGATGATCAGAATATCATAATATAGGAGTATACTATTTTACTGGAATC
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AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT
TAAAAGAACAGGAAATGAGAAGAGAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA
TATACTTTTGGTGTGGATCCATGTGTATTACTGAAATCATCGAAACGAATATAACCTCCTTTTC
CCACATTGACATAACTCAGACACAATCTTTCAAATAAAACATGTAATACTAACTATTATTTTTTTT
TCGTATAGGTTTTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAAT
TGAAAACTTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA
TCACCACCTGTTTTAGTCACGCTCAAACTGCTGTCACTTGTGACTCTTGTCTACTGTTTTGTGTA
CCCCAACTGGTGGTAAAGCTAAATTGACTGAAGGTTGTTTCATTTCAGAAAGAAAGTAA

YHR021C_homolog 82aa (SEQ ID NO 366)

MVLVQDLLHPS PATEAKQHKLKTLVQQPRSFMDVKCQGLNITTVFSHAQTAVTCDS CSTVLCTP
TGGKAKLTEGCSFRRK

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; exon 1:
501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
TTTATATTGTTTTTTTGTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTTCATGTAATT
GTGATGTATTTTTTTTGTGGTCCCTCTTTGTGTTTTGATATTTTGCAGCTGGTCGGATCATACAA
ATTTGGAAGGAGCTACCAAAGCAGAAATGATAGCAAAAAAACAGGAGACTTTTGGAAATTTCTTG
GTTTAGGGCTCTAGCCCTAATGCCTGTATATAATTGATTGATGCTTTAAAAATTTGTGCGGTGAAAA
ACAGAAGCGAAAAAAAAGAGCTGGAAAGTGTGATTAAACAACAACGAGGGAAGAAAAAACTTAA
TTAGGTGAACAAAAATTAATGTGTGAGCGGTGTACATGCACAATTTTCAATTGGTTATTCTCACGCA
CTAACAACTCAACCTCCATTGTGAGAAAAGAGATTTTCTTTGAAAAAAATTTACATACATATC
TTAGTTCACTAGTAACCTTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC
AACAAATGAGATACAAGATATTCTCCAATACAAAGAGATTAATGGTGTTTTGTATAGAGTGTAAAG
CCATGTGTTTAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGGAAATTTGTCCAAACAACAT
TGAAACGAATTTTCTGGGATAGCGTTCAAACAATCAAACCTATCCAGGTTTCTTATGACAATTAAG
AAAACAAGTCAATATTATCAAAGATGGAGTTTATAAGGAGAGATATTGAAACATCAAATTGTTGA
AAGAAATAGCCAACATTTGGCACCATTTCCTGTGATCATAGAAATACTAACAATCCTCTTGTGTT
ATAGTTAACGTTCCAAAACTAGAAAAGACCTACTGTAAAGGTAAAGAATGCCGTAACATACCCAA
CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTCGCTCAAGGTAAAAGAAGATATGAC
AGAAAACAATCCGGTTATGGTGGTCAAACCAACAAATTTTCCACAAGAAAGCCAAGACTACCAAA
AAAGTTGTTTTGAGATTGGAATGTGTTGTCTGTAAAACCAAGGCTCAATTACCATTGAAAAGATGT
AAACATTTCGAATTGGGTGGTGACAAAAACAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368)
MVNVPKTRKTYCKGKECRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK
KVVLRLCEVVCCKTKAQLPLKRCKHFEELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID
NO 369)
GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT
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TGACGGTGCAAAAAGATCTACCACCAAGAAGCACATAATTTTTTGAATGATTCACGAAAGAGTTT
CATAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAGTTCCCGTAATGTTTCACGGGAAGCAG
CAGCGAAGTTCAATAATAAAAATTTGATCATCTACTAATGTGGACGTGTCAACGAAACCGGAAAA
TATAAATAGCAGAGATAACAAAACTGAGAAGAATATGACTTTGAGTTTCAGAGTCAACCAACCGAG
TGTGGAAGAAGTTAGTAAATCTTTGAAACCAACAATTACCAAGAAAACCTTCATTCCTGATTACTT
AAAATCTGCCAAAACCTAAGGCTAAAGAAGAAAAGGTAACAATCGAAAAAGTGACAAAACGATTAA
TTCAGAAGAACGAAAAACGGAACCAATTCAACAAAGCGAGCAACTTTTAACGGACAAAAGGATAA
TAAACTGGAACCCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG
CTGTGCCCTAGGACCTGATAAGAACTACTGGAAAAACGATTCAGATAAATCAGAAACGACTCAACC
AAAATTTGCCCGCTCAGAATCATTGCGGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC
TGATTTCAATTTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTTCAGTTGTGGCAGCAAA
TGTGCTGGAGAACATTTGATGAGAATGAAAAATTTTCAAGAGCTGAAACTGTTATAGCAGATGACCT
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GAAGAAAACAAAATTGAATACTATTTTAGTTCCGATGAAGAGGAGGAGAGATTCAAGAACCAGA
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AGCAACAACAGAAATCAGTAACGATAAAACAGAAGTAAATAAGCCAGAAGTGAAAGAGGTTGGCGA
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TGCAAGACATCTGAAAACGGTGTCAAGTTCAAAATCAGAATCTAAGATTTCAAAGTCTGAAGAAGT
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CACATGCTTGCATGAGGCAGCATTGGAAGGTCATACACAAATTGTGAAATATCTCATCGAAAATGG
TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGAATCCGAGACACCATGATCGATGCAGCTGA
AAACAAACATCTTGATTGTGTTAAAGTGTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT
TGATGGATTACCGCTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAT
TATTCAAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTTCAGTTTGT

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACTATTTTGCAGAGCT
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TGTTGCTGGTCATAATTTAGAAGGAAAACAGATATTTTAATTTTAGCTGCTAGAAAACGGCCACAC
AGAAGCTTGTTGATATTATAGCTAGGGCTAAACCTACACCTTTTAATATTGATACCGAGTCAAGTTG
TGGTGTACTGCATTATTGGCCAGTATTGGACGCGGTCAATTTTGAAGTTGTCGATTCTTGTGTGTC
CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAGATGGGTTGAATGCTTTAGAAATTGCACAACA
CTCGCCACATTTTGATTACGCGGAAGTTAGTGTAATAATGAAATTCATGGAGAAGAAGAGTGAAC
CAAATTTTGTCTGGTATTCGGTCAAGGGTAGTATCTCGTGCACATCTCGTGCACCTTCTGTTCC
CGTATCATCAGACGAAGATGACGTAGTGAAGAAAAAGAAATTACAGCACACACAGAAAATAAAAG
TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTCAGCAATCGGAAACC
CCACGAGTCTACAGGTCGAAAACCTTGAAGAACTCATAGCAATGAGGAAAGAAAGCGGAAACGTGA
ATGGTCAGACGATGAACCTAAAGAACCACATCTTTTGAAGAAAGTCAAAGTCTGATTTGAAATTGAA
ATCACTACATAGAGAATTCACCTTCTGATGATCACCACACCAGTGAAAGCCATTGAGATTCTTTTGC
AGAAAAAGAAAACATTTATCGGCAACGCCACCTGCTCCTCCGCCACCACCACCACCACCTTC
TCAAGCAGTTATCAAGGCACAAGAAGAACAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA
AGAAAAGGTGAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAGAGAAAGA
GCAGAAACGGAAGAAGAAGAAGAAATTGCGAGCACAGAAGAAAACGAATTGCCAAAGCAAAACA
GGAAGAACAGGAGAGACTTGCTAGAGAAGCAGAAGAGAAATCGAAAGAACTAGAGAAGAAAGAAAGT
GGGGTTGCGACAACAGTTGACATTAGATCATTTATCCGGTTGGATTGCGTTATTGCAATTGATGG
AAACCCAAATATCTCGGCTGTTGATAAATTTTGCCTTTCTATGTATTTGTAATCGACGATAAAAA
GTATGCTGTTGATTTGCAAGTCTCCTTGATCACGTCAACGGTTGTCAGCAAGGTTATCAATACTGT
ACAACCTCATCAGAAGAGAGAAATAAATGCAACTGAAAAAGCAAATGTGGAAGCTCTTTTTCAA
GTTTATTGGTATTGATCCTAGGAATCCAAATTGTGATCAAAGAAAGCTCAATAACAAATGGTCAAAA
ACAGTTTCAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTAAAGGAATT
TCCAGATACACTCAAAGCAAAGATAACCAATTGATGTTAGTTAGAGTCTTTGAGTGGGTT
TTCTGATTGCGTCAAGGATGATATAATAGTTGATGGAAATCTTGAAATTGATATTGATTTCAAGAA
AATCGAAAAGTTTATTCTCCTCATTTGAATACTAGGAAAGACATTATTAGGACTGTCAGTACTTT
AGCACACCCACTATGGTGA

YIL112W_homolog 1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKKTSTFDYLSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ
SEQLLTDKDNKSEPNSEVNLDNNDSSKATAGCALGPDKNKTGKNDSDKSETTQPKLARSESFADT
SLLSPVNESDITDFNFELAEIPEAKDGSVVAANVSENIDENENISEAETVIADDLPRLEDEGKLLR
EQTADVCRHKLKKTCLNTIFSSDEEEEEIQEPDFKLQEPKLPEDDQHPDFQNSKATTEISNDKTE
VKNPEVKEVGEKERNHQLDRLPIKKEKMRSENAKTSSENGVSSKSESKISKSKLPYKVRDSSGR
SLLQRAKCKGNFADVQDYIERGASANEDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG
DSETPLIDAAENKHLDCVKVLENDADPTIFNIDGFTALTKIYNEHEGEEGYDEIIQVLEEATANY
NSRLPREVQFVSDAPIGSGPIMEDPNNDNYFAELIKGKIYKYAAENSKEKTAIEYFVAGHNLEGKPD
ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVVDLSLSKGADPFKTRKK
DGLNALEIAQHSPHFDSREVSVMKFMKKSGTKILSGIPSRVVSRASTRAPSVPVSSDEDDVVEE
KEITAHATENKSAEKKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDPEKPHL
LKKSksDLKLKSLHREFTSDDHHTSESHSDSFAEKRKHLSATPPAPPPPPPPPPPSQAVIKAQEEQK
IKDAEEARLWQEKVEAKKRARREMLKSEKEKEQKREKEELRAQEEKRIAKAQEEQERLAREAE
EKSKELEEKVGLRQQLTLDHYPVGLRYCKFDGNPNISAVDKFLPFYVVIDDKKYAVDLQVSLIT
STVVSKVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCQDQRSSIINGQKQFQNLHLHVE
VDLAEFLKEFPVHSAKADNQIDVSLESLSGSDCVKDDIIVDGNLEIDIDSKKIEKFIPLHNT
RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCCTCACTCATGATTGATGATTTGCCCACTAAAAAGAAAACCAAT
GAAACAATAAGATTGATTGATAGATTTGGTTGTAATTAATCTGATGCTTTCACATTTGTTTTTGT
TCGTGTCCTCGTCATTGAGGTTGGGTAAATTGTTTTTCTTTTGAAGATTGTGAGCATGCAATGTCG
CATGCAAATATGATGTCGCTCAATTGCGACATACTACTTAGGGCTATAGACCTATTGCACGTGCGT

TAGTTTTAAACCTAAAAAACAATTTTGTGCAGTCGTGCACCATTCGTTCTATTTTTCTACTGTGA
TTGACGTACAAACCTTCACAGTTCACGCACACTTTTGTGCGATTCTCAAACCTCTCTCACAGGCTTG
GTAGGAATGAAAAAATTTTGGTAAAGGCCAAAAAATAAACTTGAATATTTTGGAAATC
CCTTTTTTGATTACTACAATAGATTAAAGTAACTAAAGATGATTGAACCATCCTTGAAAGCTTTAG
CTTCAAAATACAACGTGTGAAAAATCCATTTTGTGCGTAAATGTTACGCTAGATTGCCACCAAGAGCCA
CCAACGTGTCGTAAGAGAAAAGTGTGGTCACACCAATCAATTGAGACCAAGAAGAAATTGAAGTAG

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)

MIEPSLKALASKYNCEKSICRKCYARLPPRATNCRKRKCGHTNQLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:
501..2294 (SEQ ID NO 373)

ACTCAGCCTTTTGAATTCACCTTTTGGTAAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT
CTAACTCCATATTGTTGTTCTACCTCTTGGCATAGAGACTTTGATCGTGACATTTTGTAAAGTGG
TAGAGGTATGGGTAAAGATTATTTTACCACCGTTTTCTTTAGCAAATAGTCTAAAGCATTTTCTG
AATGTTGAGTTTCCGTACATCATAGCTATCTTTGTACAATTGATTTGCTTCTACCTCTAGTCA
TGGAATAACAAGTTAACAGCGTGTTTTGTGGTTTGTGGAAACAAATAAATTTGTGGTGTGTAAT
GTGTGTGTTTGTTTTTTTTTTTTACCAGCATTTTGTCTTGTCTAAAAATGAAACAGCGCAATGAT
TCTTTTCATAGTTTTTTTTTTTCCATACATAACTCTGACGCGTGCCTATATCTGCTAACATACTC
GGCAACAACAAAGAAAAGAGAATTTGAACCTAATCCGAAGATGAACGACCCAGAGATGAACAAATTG
ACTCCGATGATGTATTAACAGAAGATTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTTGAAT
TGAAATATGCAGAATTAAGAAGAACAAGCCTTGAAAAACGTCGTTACAGTCCACTGGAAG
ACATGCTGAATAAACAGAAACCCCATCAACCGGAGGTCCCAGAACCCAGAAAAAGCTAAAGTCC
ATTTGGATAAGGTAGTAGAAGAACCAGCAAGAATTTTACCAAGAAGGAGCCTCGGGATTCCA
AGATAAAAGAATCAAACCTCTTAAACAACTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG
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AAGACGTTGTTGATGATTTAGAACCGATATCCAAGCTTTACTTGGCAGAGAAGATACCTTGCCCAAC
TGCAAAATTGCCGACATTATTGCCGAACTGATAGCAACATGAAATTCCTTAAATTTGACAAGTTTT
TAGCGAAAACCCATAAATCAAACAACATATGCTGAACCCAAGTATTGTAATTGGTGTCTTGTTCCT
TTGTGGTGCAGCAAGGACCCAGTGCAGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGGTTG
GAAATTTTATGAATTCTGTAGACTTGATGCTTTTTGTAAAGGCTTTTCAGAAAAACGGGAAAATCC
AACCGGTGATTTATTATTCATTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG
GCCAGTTTCAGTCTGGGTTCAATTTGAAAGTAGAAAACACCAATGTGTCAAGTATTTTAGAGATAG
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GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAATCAAGCGGCGCA
AACTAATAGACGACAAGGCAAAGGAGATGCTTGAACAAAAGCTATCGAAACTAGGTTTCGGCTTCAT
TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCGAGTGATCGTCTGAAGA
GCAAAGGATTCACCAACACAATGATTTACATATTTGGGTTTGATCCAACAGGTACATCTTTGAACC
AAAATAGTACCCTGCTTGGCAGCAAGCTGATGGAAAAATCTCGAGCACGGGAATTGCATGATTTGA
GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA
AATGGAACACGAATATCAGAATTTACAAAATTACGATCGACGAGTTGCCAGCCACTCCTTGAGTA
CCTCTCGTCCGTTACAGAATCTTGTAGGAAAGCAACACACGCTACACTAGTAGATAAAAGGAAAA
GAGTGGTTGTCTCAGATGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTTGAAATCCAGT
TTGACGACGAAAAGTCTAAGATGTCTACATGAAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)

MNDPRDEQIDSDVLTEDSSDELKDLVQEFELKYAELKKNKALKKKRRSQSPSEDMSNKQKPHQPEV
PRTPEKAKVHLDKVVEEPKQRIFTKKEPRDSKIKESNFLNKLYETSNKHKEDAHKIDFSKRREFE
QLDKYTFTPKDVVDLEPI SKLYLRRRYLAQSQIADI I AETDSNMKFLKIDKFLAKTHKSNNYAEP
KYCNWCLVAFVVRKDPVQVAANN SKYIKLVGNFMNSVDLMLFDKAFQKNGKI QPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGFCFKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFKSSTRMELNGSVSIRSPQKNKKKMYMKNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK
VLQNIKRRKLIDDKAKEMLEQKLSKLGASLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG
FDPTGTSLNQNSTSLGSKSMEKSRARELHDLVETSGHKSLSSSKQDRQSKVAKWNTNIRTLQNYD
RRVASHSLSTRRLQNLVKGQTHATLVDKRKRVVVSDDEQPGMEEDEEDIEIQFDEKSKMSYMKM
TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496
(SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTGGTTTCGTTTAGGTG
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TATAACAGAACTACCAAAAGTGAGCCACATCTGTTAATCTTGAAAAGCAAATGAGAAAACCAT
TTATGCAAGTCGTGTAAGTGTATATTCTTGGTCAATTGCTACACTTTTGTAATGAATACTGTAAT
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AATATAACAAAATGTTTCAATGTAACTGATGGTTAAGGGATTATAAATCAAAGTGTAGTGTCTT
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AGCAGCCCTCCGGCAGTGTCAAATTAAGAGGCATGGGACACTTGGTTGGCCAGTCTATAGATGTGG
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CTGCTTATGCCAGCCAGTTTTTTTGGAGTATCGTGCAGTGTGGTGTTCCTGAAAGTTTGAAGCCAA
CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG
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ACCCTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAATCATCGATCAAA
AGCAATTACCAACTTTGATAAAGTTAAGGGGTCATTTGTTCCGTAGGAGGGGGTGGCTTATACA
ACGGAATAGTTGAAGGTTTGGAAAATCATAAGGAGATACCAGTGTGGCAATTGAACTAAACAAG
CGCCACGTTTTCACGAGGCGGTCAAAGAAGTTAAAGTTGTTTTCATTACAAAAGTGCAAACCTTGG
CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAACTATATTGAGCGTCTTACAG
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ATATGGTTGAGCCTGCATGTGGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA
AATTTGGTACATTAAGTCCAGATGATATTATCATTGTTGTCATATGTGGTGGATCGGCTATCAACA
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)
MKEPSITTTTVEVTDKLPKPPCRVFFKNEYEQPSGSVKLRGMGHLVGQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFGVSTVVLPESSKPTVIEKLKSLGADVIIHGKHWEADNYLTFDVIKNL
DKTVYPVYCHPFDPLWEGHSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVHLQKVQTLATSLASPYLSSKALANYIERPTVLAIEDDLDAVKG
VVDVYDHFYGMVEPACGASVASVMHRQDLNKFGLTSPDDIIIVVICGSAINKYIIDEYRSLLEK
DS

YJL034W_homolog 2564bp PathoSeq: 1..806/1401/2504, public:
807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)
TTTTTGAAAACAGAGAATGAATGAACAATTGATGACCATAGAAATGAAGTGAGAACACATAAATCT
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TTTGTGTTGTTCAAGCCAAAAAAGAAAGACAGAAACAGAAAAAGAAAAATCTCAAAGTTGCCACGT
AAGCACAATTAATCTTTTTATGGTTGTAACATATTTCTAGTATATTCTACGTAATAGGTGAGGTCTT
ATATGCAGTACACACAGGTTTTTTTTCACAGATGTTGACACAGTGTGAAAATTATTACGTTGATT
TATAAATATACAACCTTACCTTCCACGTTTTTTTTTTTGGATTGTTGATTGTTGATTGTTGATTGTT
TTTTTTTGTCAATTTATTTATTAACAATCTCTTGTGAATACTTTATTTGATAAATTTTACAAGATT
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ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

ACGCTGCCAAGAATCAAGCTTCCTCTAATGTCAACAACACTGTTTTTCGATATTAAAAGATTGATTG
GTTTGAAATATAATGATGACACTGTGCAAAAGGAACCTTAAACATTTGCCCTTACAAAATTGAAAATA
AGGGTAACAAACCAGTTGTTAAAGTTGAATACCAAGGTGAAGAAAAAACTTTCTCCCCTGAAGAAA
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CTATTGCTGGTTTTGAACGTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCCTATGGAT
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GTGAAGATTTTGATTTCAAGATTGTCTAGATACTTGGCCAAACAATTCAAGAAGAAGCACAATATTG
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TATCTTCTCAAATGAGTACTAGAGTTGAAATCGACTCCTTTGTTGATGGTATTGACTTTTCTGAAA
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AAGGTGTTGATGACATTGTTTTGTTGGATGTTAACCATTGACTTTAGGTATTGAACTTCTGGTG
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ACAACAACGATTTGGCAAAATTCGAATTGACTGGTATTCCACCAGCTCCAAGAGGTGTCCACAAA
TTGAAGTCACTTTCTCATTGGATGCCAATGGTATCTTGAAGTTGAAGCTGCTGATAAGGGAACCTG
GTAAATCTGAATCCATTACTATCACCAACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA
TGGTTGAAGAAGCTGAAAAATACGCTCAACAAGATCAAGAATTGAAAGAAAAGATTGAAGCTAGAA
ACTCATTAGAAAACATATGCTCATGCTTGAAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTAG
GTTCTAAATTGGATGACGATGACAAGGAACTTTGGATGACGCTATCAAGGAACTTTAGAAATTTA
TTGAAGATAACTTTGATACTGCTACTGCTGAAGAATTTGAAGAACAAAAACAAAATTAATTGACG
TTGCTAACCCAATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAAGGTGCTGGTGGCGCTGGGG
ATGCCAAATTCGGTGATGATGATTCAGATGATGAATTCGATCACGATGAATTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)

MRSSQSSWLPRIGLLYVALVILIPLVSPKHFAVA AVSDDESSTDNYGTVIGIDLGTITYSCVGV
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAKNQASSNVNNTVFEDIKRLIGLKYND DTVQKEL
KHLPHYKIENKGNKPVVKVEYQGEKTFSP E EISSMVLGKMK SIAEDYLGKKVTHAVTVPAYFNDA
QRQATKDAGTIAGLNLVRIVNEPTAAAIAYGLDKGDQEKI IIVYDLGGGTFDVSLLSIEGGVFEVL
ATAGDTHLGGEDFDFKIVRYLAKQFKKKHNIDITANSKAI SKLKREA EKA KRTLSSQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLPVEQVLKDGGVKKS DIDDIVLVGGSTRIPKVQELLEG
FFDGKKASKGINPDEAVAYGAAVQAGVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNNRLGKFELTGIPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEA EKYAQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFD TATAEEFEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDSDDEFDHDEL

YJL035C_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:
501..1343 (SEQ ID NO 379)

GCCCCATGGTGACAGAAAAGTATTGATCCAGGTTTCTTTGAAGGTTTGTAATACGTTTTAACTTG
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AAGATTGTCTCGTCTTCAGTGTTTGCAGTGGAGCTGCTATTGCCAGTCGGCGGCATAACAGCAGGT
TCTGGTATGTCTATCTTCTACTAAGCCGGACAATCCCAAAGCCGCTCTCTGTTCTTTTATTCTT
CTAAGGAATGCTTTATGTAGTTCTGACATTCTTGCCTAAAAGGAAGTACAGTATTAAAGCTCGAAA
CTCAATTGCAACAAAAGTCTTAATTTTTTCTTCTATAAGTAATTGATCTTGGTCCCCCAACAAAA
AGATACAGAGGAGAAAGGAGGGCCTTAGGCTGACAGAAAAAAAATTTAGTACCTGCCACACCAG
TAGCTCCAAACCCATATATGATTTGATAGAGTTGAAGTATGCTGACAGATCTTACTTCACACTTTC
AGTACATGGCTATAAGCTTGTTCGTTTACAAAGCCTTACTAAATAATGAGACACCAGTGTCAT
GTATAGTCGTGGATTCAAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCACTCTC
TAAATGGTACACAACACGCAGAATTTATTGCTTTACAACGATTTGGGGAAACAAAACCTGAGTATTG

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
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TATCAATACATAGTGACATCACCTTGCCTAACGCAGCTTATTCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACATATTACGAAAATTTTATATTCAACAAAATGAGTCGGCACCAAAATCCAAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTTGTAGCATTTCAAAGG
ATGAATTTATAGAGTTTTACGAAATGAAAGAGTGCATATTTACGATGGGAAGATTTTGAATCA
CTCCATTACAAAACAAGGGTTATGATATAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAAATAATTGAATTTACACAACCTATTTT
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAACCAATAGGCAAATATAACAGTAAAAAGA
GACACTTTGCAAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)

MSTDLTSHFQYMAISLFVGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVEPCIMCASYLRLGLIKKVIFGCGNDRFGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQQNESAPNPKIKKNTDIESKEYPENQFCSISKDEFIEFYGNERNVH
IYDGKIFEITPLQNKGYDIKELISLDMMQKVPFLEDELGQITDEQIIEFHNLFNINDDGTVNYKK
PIGKYNSKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;
CDS: 501..>1502 (SEQ ID NO 381)

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ATCAATTAAAAACCTTACTCCATCTTTAGGAATAAATAATACCATTGAATCCAATATACCTTCAG
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AATTACCAATCAATAAAAAACAATTGGCATATTTAATTGCTCATGAATGGACTCATTTACCTGATA
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AACATTTGAGTGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTGGAAGATATTAAATTAC
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TAGAACTATTTATCAAACTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C_homolog 334aa (SEQ ID NO 382)

MLRFTRTTAWKLRSIPIATIYRQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW
KKEVKNFNNETQKYEIQLDGKTLRPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSSTLPLTAL
ATRAIDLSSQHLSDMKTEKAEEMLALEDIKLQMLRYLDTDTCLIFATNKECDGKLRKRQEIIYRPL
INEFNEFFTIIYAHNKNLIPRQKSIELKYLDCE TDGLRGNKQDETTQLVVDWLNQLPIYDLIALEK
TILTTKSFLCGITLLRSNVNDIETLKELYQFNKNSIDEDYYHKTLEELVELGNLETIIYQTEEWGEV
EDTH

YJL187C_homolog 3689bp public: 1..452/3414..3689, PathoSeq:
453..3413; CDS: 501..3686 (SEQ ID NO 383)

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AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAACAATCATCCAAAGTTTAAA
CAAAGTATTCTTTTTTTTTTTCAATTTTACAACCAAAGATAAAATACTACACAACACCCAACATTA
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CGGGTGATACCAGTAGCACACCAATGGCCAACAATAATCCACTAATGACAGCACAATCTCCTCTC
AGAACCATTCTAAAACGGCTTGAGAAAACACCAACAACAACACTACCACCAACACCTGCACCTGC
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ACGATAGTATCGACACGTTTCTTGATAACTCCAACACGGAACGATAGAAGATGGAGAGCTCACAA
CAACAGACGACGATCAGGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGCAGTACACCC
CAACTTTGAATATCTTGAAATCCAAAAAGTCGATAGCTTCAATATTATATCTAGCAAGCATAGAA
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CGATGGCTACAATAAGGTTATCTAACAACCTCACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA
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GACCACAAGAAGATTTAGAATTAGTTTTCAATTCGTGACATTGAACTAGATGATAACATAATACCAG
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MDSNPCQDVSGDTSSTPMANNPTNDSTISSQNHSKTGLRKHQQQHYHQSHSQMHSQSQQSPYIN
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 GSSDRKLPPETPIKRNPLMILNTNKVVPYSSGFAEGKDVMDQHDYSHIPCQNQRFPGSVNPNT
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 IELDDNIIIPETPTKSLLPNQHHQHHLPLYTQSKSPLLKFDTEKDGRRLSIVLDKSNATKREISE
 PPSTPINMSFAKNSFKKPMNNAERGDDPDSIIAQRIDIMPSLDEVD SVSVYP SKIDEHLIEKFGMK
 NIKYIGSGAFSIAFECLFNNEKFAIKRTTKPLIGKLEKQTIKREIEALRVLT SIKED EATNMQEQE
 EGKEYLVYFIEAWDFNNYYYIMTEFCGGT LDFLEENKHYKIDEFRIWKILIEILNGLKFIH SKN
 YLHLDLPANIFITFEGLKIGDFGLATKLP ILEKDFDLEGDRNYIAPELINDKIYTPFADIFSLG
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 NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:
 501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)
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 AGCATTTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTCTAGTCATGGTTGAATTGTCTGT
 TGATAAAAAGAAACCGTGAAAAGGAAGTATTTGTGAAAATCGATTGATATTTTTTTTTTTCCTCCT
 TCCTCACTGTAAACAGTAGTAAACACACTAGTTACAAC TGATGACCTGCATATTATAAATCTTTCTG
 AAAAAATTTTTTCCCTGTATTTTTGTAAATCTTTTCGCTCTTTCTCACTCACTCACACTTATTAAT
 GAATGAAAGGTTTGGTGTCTACAACTCCACTAACAAAATCTCACTCCTGTGCCTAAACACACACA
 GACCCACACGCAAACCTTTCTCTCAGAAACAGAAAAAAAATTTCAAGCAAAAATTTTTTCCATC
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 AATGATGCTTTTCAGTCTTTTATTGGGTGATTATTATAATAAATGGCAGATGAGAAATATATTGGA
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 TGCTGGAACAAAGACGAGAGAACTAGACAACCTCAGATATAATAGAACATCCATACTAACTTCACTC
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YJL189W_homolog 51aa (SEQ ID NO 386)
 MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRTDNKIRYNAKRRHWRRTKLGI

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ
 ID NO 387)
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 TGTAGACACCAAACCTTTCATTCATTAATAAGTGTGAGTGAGTGAGAAAGAGCGAAAGAATTACAA
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 GTTTACTACTGTTACAGTGAGGAAGGAGGAAAAAAAATATCAATCGATTTTTTCACAATACTTTC
 CTTTTACAGGTTTCTTTTTATCAACAGACAATTC AACCATGACTAGAACCTCCGTCTTAGCTGATG
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 AAGTCATCATAAAATTCCTTGACTGTCATGCAAAAACACGGTTACATTGGTGAATTCGAATACATTG
 ATGATCACAGATCCGGTAAAATTTGTTGTTCAATTAAATGGTAGATTAAACAAATGTGGTGTCAATC
 AACCAAGATTCAACGTCAAATCAACGACATTGAAAGATGGACTGACAACCTGTTGCCAGCTAGAC
 AATTCCGTTACGTTATCTTAACCACTTCTGCTGGTATCATGGACCACGAAGAAGCTAGAAGAAAGC
 ACGTTTCTGGTAAAATCTTAGGTTTCGTTTACTAG

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLTVMQKHGYIGEFYIDHRSGKIVVQLN
GRLNKCQVQPRFNVKINDIERWTDNLLPARQFGYVILTTSAGIMDHEEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public:
3042..3259; CDS: 501..4616 (SEQ ID NO 389)
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CTTATCCTTCTGTAATTTCTTGATCTCTGTTTGAATCAACAACGCTTTGTGTTCTCTTTCTGCC
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CAACAATGTGCGATAATGAACTCCCTCAAGGTGAATCCAATGAACAAACAGGAGATGACTCAAATG
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TCAACAAACAGAGAGAGTTATTAATGTTTCTACACACAAACCTACTTTTAGCGATTTCAAACCTT
TATCGGACCAATTATCAGAATCAAAACGCAACTATTATTTTTATCCTGATTATAAAAAAGATGGATG
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CGGGGTGAGAAAATAGTAGTAGAGCACTGGAAGAACAAGATGGATTTGTATTAATAAATAAAGAGG
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GGTATTATTTTAATGATAGTCGAGTCACTGAAATTAATAATCCTCAAGAAGTCGTAGCTAATTCTG
CGTACCTTTTATTTTACCGTCGAAGAAGTTTCAAGGAGCTGGTATTTTGGGAGGAGAAAACTTTA
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AAAATGTTGGCCAAATAGTCAATACGTATGCCAAAATTGAACAAGATATAATTGATAAAGAAACAG
AGAAACAGAAAGAGGAACAAGAACAGGAACAGGAACAGGAACAGGAACAGGAACAAGAGCAAGAGC
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YJL197W_homolog 1372aa (SEQ ID NO 390)

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HHGHHDSPIPVLLSKTSTFHRLMDVIRYNVLKAPRKSTKDFRIWFIVPQDKGLQYLI SIQTFMFD
ISKKTLLVSPNMLEDALKDHGIVASSYNIMVEAKEKHQTEFPIDQFILSHSNAYEEVVSQGGHGLGLS
NMGNTCYMNSALQCLLVPEINYYFFYNIYKKELNFDNPLGYHGDVANAFGSLLKQAFDHVKNSSS
ISPREFKSTIGRYSSMFSGYLQQDSQELLSWLLDALHEDLNRIHQKPYCEKPELKDDEIDDPQAIT
KLANTCWNQHKARNDSVIIIDLFTGLYQSTLICPCDGKKSITFDPFNDLTLPLPISKWKYHTFTIVD
LSNQGVIPERIMKLELVNKTNSNFDDLLSYLSNLFNVPSTELFAYEIFQNAIYSDFLDYTKNKFL
PISDIIRDITDDVIVYIVPHNPAVDIIVPVFNAVEDADSSYQMVNFFGIPLFVVMNKEVDVNSFGFI
RKKLLETVSLLSKIDLVD EYEKIKRSNEDYVEKVFYKKSDFPALSQPLETSDCEKNNNNTSDNDD
EDADNDEGYDSEVSLANPYLGANFGFKIMYVHDYSPKLSNLSRYSRNDQTTKFKQTERVINVPHT
KPTFSDFKPLSDQLSESKRNYFYFPDYKKMDDEMQLVEEVNQNLAEQXEARSSGSENSRASEEQ
DGFVLINKEDTLKQOSTVPAAAE TVPPPLPVRNNTGVHIPSSDEETESANLGSFLDSTSNLPLPP
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LTIHLKRFHSARAFSDKIDVLVD FPIEGLDISSYVANTDLTPEDCLYDLIAVDNHYGGLGGGHYTA
SVKNFRDDKWYFND SRVTEINNPOEVVANSAYLLFYRRRSSKGAGILGGENFIDLQKGREEYSE
SLQKKRLVLQNVGQIVNTYAKIEQDIIDKETEKQKEEQEQEQEQEQEQEQEQEPVQEPDQEQEP
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EDSNIRKQRLLSKENNSNKLVIHKSNGRQEVTSPPVPIETDGD TDVTDNSNT

YJL198W_homolog 2693bp PathoSeq: 1..899/1285..2693, public:
900..1284; CDS: <3..2690 (SEQ ID NO 391)

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TTACTGGTGAAATAGAAATATACTTCAACTTCTTCCAATGGTGAACATGACACCACCACCACCTGCCA
CTAAACATGAATTGATATTACAACAAATTTTGAAATCTAATGATGAATCATATATTAATCCTAAAT
CATTAAACATTTGATCCATTAAAAATTTTCACTAAACAATTAATTGGTGAATTAATTAATTAATC
AATTTTACAATTCAAAAGAATCGGAAATTTTCAAAATTTATAATAATTTAATTCATGATTTACAAA
ATCAAAATATTAATATTTGATGATGATTTAAATTCACCTCAAGCTTATAATTATTCCGATCCAAATA
TAATAAATACTGATGATCATCATCAATATCATTTAAATCAACTTTATCAAGAACAGTTACTAATG
CTAGTGATTTGATACCATTAATCATATTGATAATGATAATAATAATAACAACCAAAAAGA
ATAATTATGATTTGGAGAAACAAAATAATACTACAGTTGCAATTCATGATGATGATGATTCAGAAG
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AACTTGTGGTTATTCAATTAAACAAGATTTTATTAATGAATTTTACCTCAATATTCTCGAGTAT
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TATCAAATAAAATTA ACTACTCAATCAACAACTAAAGAAGATTGGGATAATATAAAAATTTGAATTAA
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AAAAGAAATCTTATAATATTGATTAGATAATTCTGTGGTTCAAATAATAAAAATGGGTGATGAAG
GTCATATAATTAAATTCAATGATGAATTTATCCATGAAAAGAATTAATTTACCACAATGCCTTAAAA
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YJL198W_homolog 896aa (SEQ ID NO 392)

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KHELILQQLILNSNDESYINPKSLTFDPLKIFTKQLIGELIKINQFYNSKESEIFKIYNLIHDLQN
QNINIDDDVFKFTQAYNSDPNIINTDDHHQYHLKSTLSRTVTNASVFDTINHIDNDYDNNNNNQKN
NYDLEKQNNNTVAIHDDDDSEDEEEEEETHSHDSVLLNHTFNVKQQLKITLKRKAITLFINLS
ELKSFIELNRIGFTKICKKFDKTCGYSIKQDFINEFLPQYSRVFENDTIEELDYKLNQIIKIYAFL
SNKLTTQSTTKEDLDNIKFELRSYLRDHIVFERNTVWKDLSLEKKSYNIDLDNSVVQNNKMGEDEG
HIINSMNLSMKRINLPQCLKKLIKDYHDIDIPQFLTTQMLKIIIVIVFIIILLAVKTFNDPVQGR
CLAVLVAAAMLWASEALPLYTTALLIPLLVTCKVCKTPGTDDPMDATKASQYIFGTMWNSTIMIL
IGGFTLAAALSKYNLAKILSSYILALAGTNPRNVLLAIMCVSLFLSMWISNVAAPVLCFSLIQPV
RSIPTDSPVAKALVLGIALASDVAGMASPIASPNVIALESMPNPNPGWKWFVAALPVAIISLILI
WVELFMTFKINNVKIKQFKPIKEKLTMKQWVFVAVTITILLWCVMQKIDGTFGESGIITCPIV
FFGTGLLKVDLDLNNYPWSIVMLAMGGIALGKAVTSSGLLKTIALALQKRIMHYDAIVVLIIFGALI
LVVATFVSHTVSALIIIPLVKEVGDSLPHPLMLIMGVALIASGAMGLPTSGFPNVTAIGMRDEV
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YJR049C_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:
501..2276 (SEQ ID NO 393)

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GAAAGATAGAATAGCAAGCAAGGTGGA AAAAATTTTTTTTTTTATCACATTCAATACTTATATCC
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CAGCAGATATCATTCAACCACTTCATCAACTACTGATAAATAACAACAATTCAACTGTGACGCAAC
CAGCGCCACAAAGCTCATCGTTTCAACGCCGAAACAATCCACAACGTTTCAATCGGAATCAACTCA
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ATCGAGCTGTAAAGAGGTTTTATCACGTTTATCTACTGATGAATTGCGTTCAGTTAAATCACATA
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YJR049C_homolog 592aa (SEQ ID NO 394)

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TVAQADGLIIATPTGSTAYSLSAGGSLVHPGVSAISVTPICPHTLSFRPILLPDGMFLKVKVPSSS
RATAWC SFDGKVRTELKKGYVVTIQASPFPLPTVMSSKTEYIDSVSRNLHWNIREQQKPFSSYLKP
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YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786
(SEQ ID NO 395)

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ACTTTCGGTCAAAGAGCTGTTTTGAAATTTGCTGCTCACACTGGTGCTACTGCCATTGCTGGTAGA
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YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)
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IKESSYVNIPIVIALTDMQSPSEYVDVAIPCNNKGKHCIGLIWLLAREVLRRLRGIIPDRTTESWSVM
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YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:
81..493/777..820; CDS: <1..1332 (SEQ ID NO 397)
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YLR088W_homolog 444aa (SEQ ID NO 398)
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DLLNTANVMTYHEQIPCAMQGMSEDRVINYSTRLQTLFRGILKLTVLGLTDEVHGCFAFSGWQIQAF
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LSSVSAVVVAGFDFRKLYFVVVVEIACAILAFVPVNQVMLVAISAVVLLPRQAFISKQAAFSLISI
ALLAVALLLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH
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YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO
399)
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YLR167W_homolog 229aa (SEQ ID NO 400)

MQIFVKTLTGKITLEVESSDTIDNVKSKIQDKEGIPPDQQLIFAGKQLEDGRTLSDYNIQKEST
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SDYNIQKESTLHLVLRRLRGGMQIFVKTLTGKITLEVESSDTIDNVKSKIQDKEGIPPDQQLIFA
GKQLEDGRTLSDYNIQKESTLHLVLRRLRGGF

YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

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GCACACAACAACTAGTTTACAAAGTAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTCTTATA
GTAGTTGTCTACTCTATCAAAAAACCCATAATTTGTCTATATAACGTAAGGATCACTATATGCTGT
TGAGTAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAAACTTGTCTCATCAAACTT
GCAAAACACTTGGAGACGCGCGCGCTTTCAACACACAATAAACAACACGAAAAATAAGGTAGAAA
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CATCGATTTCAAAAGAGGTGGCAAACATTTGGGAGGAGGGCGAAAAAAGTAAGAACTCACGAG
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YLR234W_homolog 629aa (SEQ ID NO 402)

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YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq:
828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAATTATGGCTTAGTGCCCTTTATTAACATAATTAGAGGTTACATTAATACAACCTTAAC
AAACAAGGAACTAACATCCACGTATAGGGCTTCTTATATTAATATACCTAATTCAACCTGATTAT
ATTGCTTATATACAGCTTGTAACAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTATCCCC
CTATTGTAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG
TAACGACAACAACATAACAAAAAAACATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG
CACAGATAAGATTATCAGTTTCCTTTCTCGGTTGACCTTAATCTGTTTTGTATAGACTTTAT
TTTTTTTGTTTTTGACCACACCCACTTTTTTAATATCACAGATATTTAACTGATTATAGAAAAACA
CAACAATAACCCAAATACGTTAACCCTTTTATTACATATGATAGACAATATAATCAATAATTGTC
AAATCATACTACAGCAAAATGATGATAATTTTACATCCCCCTCACGACGATGTGATATATCGACCAC
ATTCTGCTCGTGTAGCACGATATCAAGTAATAATTGCATCTACATTGGGACTCACTGCCCTATTAC
TATTTTCTATCTTACGATTAAATATATCCCAAAATATATGTGGCAAACCTTTAATCATTTGAATTTCA
GTCTACATTCGACCTCAAGAAGGAATTTACCTGAATTGCCTTCAAATTCATTATTTGGTTGGATTTC
CTACAGTTTACAAAATTACTGAGCAAGAAATTTGGAACATGCTGGATTAGATGCAGTTGTGTTTTT
TGGAATTTTTTAAATGTGCATTTCGAATAATAAGCAATATGTTTAGTATTTGCCATTATATCATAT
CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATAGTGACAACG
ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTGAGCTGGAATTC
TGGTGGCAAAGTAAAAATAACGATGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA
CCTATGTATTTACATTTGTTACTGTTTACTTTCTATTCAAACAAACCAATAGGATTATTTCTATGC
GTCAGAAGTATCTTGGATCGCAAAATTCAGTCACCGATAGAACGGTAAAAATATCTGGGATACCAG
GATCAGTTTACAGATGAAGTGGCACTCGCACGGCACATTGACCGTTTGAATATTGGTGAAGTGGATT
CTGTGTTGATTGTCAAGGAGTGGCAAAATATAAACAATATTTCAAAAGAAGGAGAAGTAATGTTT
GAAAATTAGAGGAAAGTTGGGTTGAATATTTTGAAAAAAATGGGATAACCAATAAGAGCCGATTGTA
TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTTCCAATAGGTATACTGATGATGCAGAAG
AATCACCAGACTGGGGATCTCAAAATTCGAACCTGACACAAGCTTCAATAATAGATCAAGACTCAG
AATCTGTTGAAGGAGATTCTTCTGACACTTTGAATCGCTTGTGTAATGATGAACCTGAGAACAAGAC
CAAGTCTTCGGAAAGGTTGGTTCGGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACCCG
ATAAATTGGAGGTCATAGATAAAGAGATTACCAGGGCCAGAACTAGAGAATATCCCGCCACTTCGA
CTGCATTTCTCACTATGAAAACCGTGGCTGAAGCACAAATGTTGGCACAGGCAGCTTGGATCCAA
AAGTCAATCATCTTATCACCACCTTGGCCCCCTGCTCCTCATGATATCCGATGGGATAATTTGTCTAT
TAAGTACAGACAAGACAGAAATACAAAGATCCTTGCTGTACGATATTTATTGGTATAATGAGTTTGT
TGTTGGTTTATCCAGTCAGATTTATGGCTAGTTTTTTTAAACACTAAAAGCATTTCTAAAATATGGC
CATCATTTGGGGAAAGCTATTGAATCGCATAAATGGGGCCGAACTTTGATTACTGGATTATTTGCCAA
CTTATTTATTTACAATTTTAAATATTGTGATTCGGTTTTTTTATGTATGGATTCTGAAAAGCAAG
GTTATTTATCTCATAGTGATGAAGAGTTGTCACTCGGTATCCAAGAATTTTTCTATATATTTGTGA
ACTTATTTTTTGGTTTTTCAACAATTTTGGTACCGCTCTTTTTGTTGATACGACCAAAATGCAATTTG
ATTTAGCAAGATCACTCAGAGATTTGTCAATGTTCTATGTTGACTTAATAATTTCTACAAGGATTGG
GTATATTTCCCATTCAAATTATTTATTTGGTGGGAACTTACTTCGCTTTTTAGTGAATTCATTATTTA
GGTGAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT
TACCACAACCAATATTGATATTTATTATTACGTTGGTATACTCGGTAATGCTTTCGAAGATATTAA
CTGCAGGGTTACTATATTTTATTATTGGTTATTTTGTGAGCAATACCAATTGCTTTATGCTTGTG
TTCTTTTCCACTCAACGGGCAAGTTTGGCCAATAATTTTCCGAAGAATCATATTAGGGTTAT
TTCTTTTCAAAATCAAAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT
TGGCACCATTTGCCGTTTTTGTGACTTTTACTTTTGGTGGAGTTTCCATAAACAATATATTCCTTGT

CAACATTTCATTGCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTTGGAGCAAA
TCATTGAAAACAACAATAATAAACTCTTGACGAAAGAAGGGAATTGAACACTAAATACGAATACC
CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA
ATCGAGATGGTACAACTGTACGGAAACCACCTCAATATTTTCAGTTCAGAATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)

MIDNIINNLIQIILQQNDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHLNFSLSHSTSRRLPELPSNSLFGWIPTVYKITEQEILEHAGLDAVVLEFFKMCIRIISI
CLVFAlIIISPIRYKFTGRVDEDYPDDSDNDDDDGSNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLYTIFTYVFTFVTYFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRLNIGEVDVSVLIVKEWQNLNKLFRRRRIVRKLEESWVEYFEKNGITNKSDLISLHPQVGESYRF
SNRYTDDAESPDWGSQNSNSAQASIIDQDSESVEGDS SDTLNRLLNDESRTRP SLRKGFGLFGP
KVDSINYYTDKLEVIDKEITRARTREYPATSTAF LTMKTVAEAQMLAQAVLDPKVNHLITNLAPAP
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSI SKIWPSLGKAIESHKWA
ETLITGLLPYLFITILNIVIPFFYVWWISEKQGYLSHSDEELSSVSKNFFYIFVNLFVFTTFGTAS
FVDTTKIAFDLARSRLDSMFYVDLIILQGLGIFPFKLLLVGNLLRFLVNSLFRCKT PRDYLNLYK
PPVFNFGQLQPILIFIIITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPPHSTGKVPWI
IFRRIILGLFLFQITMVGTLALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLI VNRDGTTVRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq:
948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT
TTTGTTTTATCTTGGAGAACCTGTGTGTGTGTGGCGTTCTATCTCTTTATATATTTTCTCTATTA
ATTCAAATTGAACATTTTGAAGGAAATCTTTCTTAAAAGCATCTAGTGACATAGTCTCTAATCT
CCAGTCTTTTGATTAAATATTCTTTTAGAATATCAGGTGAAGAAGTGTGGTAGTCATAGTAGTA
GATACTGTGTGGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCACTGTATATT
TTCTTTTGTCAATTCCATCTTTTTTTTTTTCTCTTGAGAAATGTATAACAGAGGATCCATCCATT
TGCTTGACAGAGAAATACAGAACACTAAACAAACATTTTTTTCATTCCTTTCTGTGTGTGTCTGTT
ATACCCCAAAGTTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG
ACATACAAGCTCTTGAACCTAGTTTCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA
TTAAATGTTGACCAACTGGTTCGACAAGCCAAAAGACATATTCAACAGATTAATTAATCTCGAAGAGT
TTGGAGATGACCTTGATTTTGATGAATTTCCCATCTTCGACACCCGGTACTAGAAAGCTTAAATGAAA
ATAAAGCTCAAATAGAAGCACAAAGATATTTCTCTTGCGAAAAACACACCAACGCCCAAGAGAATCT
TAGAAAAACCGGTGTTATCTGAGTTGGTTGAAAAACCAGTGGTGTCTTATTCCTATCAAAATAATGA
TTGAGAAATTTGAACACAAACCAAAAGTTGATTGATTTCCTTTATGTGGAACCTGAATGAAAGCTTGA
TTACACCAACTGAGTTTGCGGAAATTTGTTGCAGTGATTTAGATTTACCATTCACTATGGCTGCAC
AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTACAACCTACCAA
ATAAGGGCCCTTACAATGTTACCATTGATTTATCAGTAAACTTAAATAAACAATTATACCAAGATA
GATTTGAATGGGATATGAATCAAAATGAAGTTACACCAGAAATTTTTGCTGAAATAGTTGTTGCTG
ATTTGGGGTTATCGTTAGAATTTAAGAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG
TGAAAAAAGAAGTAATAGATGGTACTTTTGACAATGAAATGCACAACCTGCATCTAGTAAAAGGTA
TAATGTTTGAACAAGGAATTAGAATTTTCACTGAAAACAGTGTTCAAAATGGAAATGACCGTTGGG
AACCTTTGGTTCGAAGTATTGACTTCTAGTGAAATCGAAAGAAGAGAAAAATGAAAGGGTTAGAACT
TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG
GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSF PKRLANDSDNSLLINVAPTGRQAKRHIQQIN YSEEF GDDLD FDEFPS
TPGTRSLNENKAQIEAQRYSLAKNTPPKRILEKPVLSSELVEKPVVLIPIKIMIENTNQNKLIDS
FMWNLNESLITPTEFAEIVCSDDLDPFSMAAQIAD SINQIIEEYSYASNQLQLENKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIRVKKEVIDGTFDNE
MHNHLVKGIMFEQGI RIFTENS VQNGNDRWEPLVEVLTSSEIERRENERVRNLRRLKRENMRDY
DDHSRRRQAGKRRYDELEGA W

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAATTGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA
TCGCTCCTGACCATTGTTTACTATATTCAACAAAACGAATTCAACAAGGCAAACGAAAGCTACATG
AAACTAAGTATCGGCAACGTCTGTTGGCCAATTGGGGTGGTCAATGTAGGTATTCATGCAAGAAGT
GCAGCACTGAAAATAACCGGTGCCTCTAACGTCAGTAACATAATGCTAAGCGAGTCTACACGAAGA
TGGATTATAAGTATAAAGAGGTTGATTAGTTTTAAAGAGAGAGTATATAATAATGCACGTGATTAG
TTTAGTAATTTTTTGGCAGTTAGGGCTATAGCCCTAAGACATTCACACAACCTAACAAAAGGAAGT
TCTCACGCACATAACGTGTAACCCACATAAAGAAAGAAAAAAAATTTCTTTGAAAAATTCACA
TCACGCTTTAACCACCTCAACCTATAACAACCTCCAACCATGGCTAGAGAAATCAAGGATATCAAAG
AATTCGTTCGAATTGGCTAGAAGATCAGACATCAAATCTGCTATTGTCAAAGTTAACGCCAAGGTCA
ATGCTAACGGTAAAAAATTCAAACAAACCAAAATTCAGGTCAGAGGTTCAAGATACCAATACACTT
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTACAACAATCTTTACCACCAACCTTAAAAATCA
CCAACCTGTAA

YLR325C_homolog 78aa (SEQ ID NO 408)

MAREIKDIKEFVELARRSDIKSAIVKVNANVGKKFKQTKFKVGRSRYQYTLVVNDASKAKKLQ
QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron
1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCC CGGGGAGCTAATTATACCCCTCATT
TTTGAACCCACCAAATTTTCTTTCACATTATAATGAAATAAGAGTATTCCTGGCTTCTTTTTTTTT
TTTTTTTTTGGCAATATAGAGAAGACTGTAATAAGTATAGCTCACTAAAAGTCTTTTTTTTTCTATT
CGTTTTATATTTTTTAAAGAAATTTGATGTTGATTTGGTAAATGCCAAATTTTAAATGTGTGTTAG
GGCTATAGCCCTAATGTACTGTATATGCAGATCAGAAATACTTTTGTACGCACAGTTTGTCTTA
CCAAATACATTATATATATATATTTTTTTTTTTTGGAGTAGAGGAGCTACACTAGACCTTAGTGCG
AAAAATTCATCTCTCTATACACTTACTCAATTTGAAGATATTCAAATTTTTTCAAAAAAAATTC
CTTTTGGATCGATACTAGATAGCATATAATCATCAAAAATGGCCAAGATCAGTCAAGGTATGAAAT
AGATATTCAATTAGATATGGAGAAAGGAAGATAAAAGGAAAAAGAAAAAAGAAAGAAATAA
AGGAATATATACATTGAAAAGGAGATAGAACATCAAACAACAACCATTAAGAATTAAGTTTAAATAC
AGTTTCAATAAAGAGGGTTTTTTTCTCAGAACAAACCATTGACTGAAGTACTACCAAGAAAGGTA
TAATGATTTTACGATTTACCTGAATATAGAAACATCCTTAATATTGAATTTCAATATTAAAAATA
CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTTCAAACCTGTTGAATGGAAAA
CTTGA AAAATCAAATCAAATCAAATCATAACCCCTCAATATATTCTTCTCTTACTTTTCTCT
ATTA AAAACAAAGACTAAGAAACATTCAAGTAAATACTAACA AAAATTCATTTATATAGACGTTTC
TTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATCAGTTGAAAGAAGAGTTCTTTT
ATCTGCTCCATTATCCAAAGAAATTAAGACAACAATACAATGTCAAATCTTTGCCAATTAGACAAA
TGATGAAGTTTGTAGTTGTAGAGGTTCTAAAAAGGTTCTGAAGGTAAAGTTAATCTGTTTATAG
ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAGAAAAATCAAATGGTGCTTCTGTTCGAAT
CAACATTCATCCATCTAAAGTTGTCAATTACTAAATTTACATTTGGACAAAGATAGAAAAGCTTTGAT
TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRSKARKAYFTASSVERRVLLSAPLSKELRQQYNVKS LPIRQNDV LVVVRGSKKGS
EGKVN SVYRLKFAIQVDKLQKEKSN GASVPINIHPSKV VITKLHLDKDRKALIQRKGGKAE

YLR393W_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;
CDS: 501..1628 (SEQ ID NO 411)

TTCATCTTTTGAAATCTTCCCTCTTGGAAACGACCAAGAGTTGGATTGCGGTGCCCTTGACTAGCAC
AACTTTGTTCAAATCTTTATTGAATAATGCAACACCACGAACCGGTATGGTCGATTTATATTTTCC
GAATTTAGATAATGCTTCCCTGTGGGTCACCCCATTTCCAAATAAGCGGGCATTTCTCTAAAATCTT
TGTACTGAACGTCTTCATCTTCATGCTTTGCAAAATCGGGATTCAACTGACGAACAAAGTCAGCATA
AAACCATTTGCTTCCCTCAATCTGAAACATTAATCTTTCAATGGAAGATAAATCCTCTTCGGGAAC
ATTCACCACAACTAACTAACAATCTTCAACACCCGATCTAGAGTTTGATTAGCTAAACCATT
GCGTAATTGGATCGACATATCTTGTATTCTTCTATGATTAATCTTTCTTTTTTCTTTCTTTTCTAC

TGAATATTCGTAATTAAAATTGATTCAAAATTGTATTGATGTTTGTATACTGGATAAACAACTTGT
GTGAGATCATTCAATGTATTTGCTGGCGGAGAAGGAGGCAAGGACGAACCTTTTTTTCCTTCATACT
TTTTTTTTTCTCTCTCTCTTTTCTTTTCAGTCACATTGTCTGAGTGTTAAAGGCTGGCTTTTCTGTG
CTGAACTTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAAGAATTTTGA
AAAACCGTGGTTTGAATTCGACCACAGATTGGTTGGACGACAAAATGCAAAGTGATTTCATCCGGA
CTTTTGTCTACCTCAAGAATAGAGTTCACGCGGTACCAGCCGCGTTTTGTTAATACCATTAAAGAAA
CGGTCAAATCGGCACAAGAAAAGTCGTACAGTATTACTAGACCATTGGGGTTGTCAAACCAGTTT
TGTTAAATCATAAATTGTGACACATACTCATTGTCCAATATATACGAGGAGTTGTTTGGTCAAA
AATCCAAAGAAAGAAGACAGAAAACACTAGACTACGATTTGAAACACTCGCCAATTTATGAAGTCA
AGTCATTTGAGAATACAAAGGGGAAAATATTTACTCCTCCTGTTTCGTACTTTTCGACAAGACAAAT
CTTTGTATTTCCCGGATTTTATAGCGAAAACATTGGCAGGTAATCAGAGAAGTTTGTACGACTCAT
TAGACAATAGATTAAGCATAGTCAAATTTGTTTCTGTTGCTGGTGAGCAGTGTAACCGTTTCGT
ACTTTAAGGTTGAAAACAAAGATTACTATTCCCAGGATTATGATACCTTTGTGGAGGAATATCCCC
ATACCAGATACTTGATGTGAATATGCCGCAAAGTTGGATCAAGGGGTTTGTGACAACTTGAGCA
CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTTCATCTTGCCTGGCC
ACATAATGTCAGCGGAAATTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTTATA
TTGTTGATTTCGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT
TGATGTGGAAGGTTGTGAAAGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412)

MFVYWINNLCEIIQCICWRRRRQGRFFPSYFFSLSLFFQSHCSSVKGWLFCAEPCGSVNARHRV
IFGETKRILKNRGLNSTTDWLDDKMQSVFIRTFATSRIEFQRYQPRFVNTIKETVKSQEKSYSIT
RPLGLSKPVLLNHKLSDTYSLSNIEELFGQKSKERRQKQLDYDLKHSPIYEVKSFENTKGKIFTP
PVSFYRQDKSLYFPDFIAKTLAGNQRSLYDSLNLRLSIVKLFSSVAGEQCTRSYFKVENKDYYSQD
YDTFVEEYPHTQILDVNMPQSWIKGFVTNLSTGNLRLKTLKPASRYENYFILPGHIMSAREQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKLMLWKVVKGVMQREMTK

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS:
501..1268 (SEQ ID NO 413)

CCAGTGCGTTTTGTTTTGTTTCCACATCATACACTTCACTGAAACTAAATAAGTTTTGTTTACATTTT
GAGACTTCAGGTACGACCCAGGGTTGCGACAAAGTTTAGGTAGTTTGTGCTCTGAATGTGCGCAACA
AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGAATTGCTGGTGCGCAA
AAAGATTATGTGTTATTTTATGTGCGTTGTTATCCTGCACACTAAATTGAGCAGTGACACACACA
CATATTGGGCTGTATTTTTATTCTTGTTTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT
TGTGTGTGCTGTAATAGTGTGTGTGTTCCAAGTCCCAGCTCTCACAGATACTCACGCACGCCCATA
CTACTGAAAATTTTCTGACTTTCTGTATCTAAAAATTTTTTACTAGGAATTTTTTCTTTTACGTT
TTTCACTTGTTCATATAATCACCAACTCAAGTACAACATGGCTGTGCGTAAAAACAAGAGATTGT
CCAAAGGAAAGAAAGGATTAAAAAAGAAGGTCGTTGACCCATTCCACAGAAAAGATTGGTTTGACA
TCAAAGCTCCAACCACTTTTGAAAAACAGAAATGTTGGTAAAACCTTTGATCAACAGATCTACCGGTT
TAAAGAATGCCGCTGATGGCTTGAAAGGTAGAGTTTTCGAAGTTTGTGTTGGCCGACTTACAAGGTT
CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAAACTTGTGTA
CCAACCTCCATGGTTTGGATTTCACTTCTGACAAATTAAGATCATTGGTCAGAAAAATGGCAATCAT
TAGTTGAAGCTAATGTCACTGTTAAAACCTCCGACGATTACGTTTTGAGAGTTTTTGCCATTGCTT
TCACCAAAAAGACAACCAAAACCAATCAAGAAAACTACTTACGCTCAATCCTCTAAATTGAGAGAAG
TCAGAAAGAAGATGATTGAAATTATGCAAAGAGAAGTTTCCAACGTACTTTAGCTCAATTAACCTT
CCAAATTGATTCCAGAAGTCATTGGCCGTGAAATTGAAAAATCCACCCAAACCACTTTCCCATTTAC
AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTCAATTATTGG
CTTTGCACGGTGAAGGTTCAACCGAAGAAAAAGGTAAGAAAGTTTCTTCTGGTTTCAAAGATGTTG
TTTTAGAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414)

MAVGKNKRLSKGKKGLKKKVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF
EVLCLADLQGSSEDSYRKIKLRVDEVQGNLLTNFHGLDFTSKLRLSLVRKWQSLVEANVTVKTSDD
YVLRVFAIAFTKRQPNQIKKTTYAQSSKLREVRKKMIEIMQREVSNCTLAQLTSKLIPEVIGREIE
KSTQTIFFLPQNVHIRKVLLKQPKFDLGLSLALHGEGSTEEKGKKVSSGFKDVVLESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)

TGATATGGATTTTTTCAAACTAAGAAACAATACCAACTACAACAACAAGAAACATAAGTGTGCT
TAATTCATGACCTCGAGTCATATTTCCACGTTTTTAAGTATGAGTGTGTTTACGAAGTTGTGGATCC
TATTTTAAATAAAACAATAATAGTAATAAAAAAAAAAACCTTCTTTGCTTTTCGAGAATTTGTAAC
ACATTGTTTCTTTCTTTCCACAGCAACCAAATTTTATTTTATTTTCTTTTGGGACTTACCCACA
GTTGCTCAATTATGTATAACAAGGGTAGAACTCTGTGGGATTCCCTCCTTAAAAATATAGCAATC
CTTTTCTTTCACAACGATTGCTATATGACCCCCCCCCCTAAGCATTCATTGCTTTTATATATATTTA
ATAATGTATTTCTCTTGTTCAGGATAATTATCACTATTTGTGACGTTTAAATTTTACATTTCTTCT
TCTTCTTCTTCTTATTTCAACATTAAGAACATTTAATATGTATTTCCCAATCATTTGTATGGTTAT
ATGTATCTATCACTTTTGTGGTTGCCAATTATGGTTTGTATCAATGGACAAATGATGATTTAAAAA
AATTTTAAAAAGAAGTAAAGTTGCATTCATGATGCCTTGGAGAATCCAAAATTAATTAGTTTGG
CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAAATAACAATT
TGAATCCTCCAGATGATTCATTAATGATTATTTGAATTTTGATTACTTATTTGGGAAAAGAAAAG
AAAATTATTCAATTAAGAATGGATTTTGAAGTTGGCCAGTAACCAGTTGCAAACCTTTTTTAA
CTCAAAATAATATCCAATATAGTGCAAAGGATACCAAAGATGATTTAATCAATAAGGTTAAAGATC
AATTTGATTCTATTTCTAAGAAAAATCATGGGTCCTAGTTTTTATCCTGGCAATTGGTTATATGAAT
CTTGGTCAGAAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA
CAAAGGATCAATTGGTTGAAAAATTAAAGAATTTAGTTATCAAGCCACTCATTCAATTAGAGATT
CCAAAGAATCTTTATTTGATTTCATTGGATTATTTGATAAAACCATTTTGTGATAAAAAAGGTCAAA
TTGAAGATGAATTTTCCAACTTGGTCATATTTCTCAATTACGTGAATGGCTTTATTTACATGGAT
TTATTGACACTAAACCAGGAATTTACGTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCCC
AAAGTTATAAGAAATGTTTGTGAGTGACATTCATCTTGGTTGGCAAACACTGAAAAGAAGTCTC
AACCTTGGATCACAAGGGAGAACAAAAGTCTCAGAAAAAGAAGGGTAGTAATTTGATTAATGATA
CATTCTTTGTTGGTATTAATAATTGGTCCAAGGATAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C_homolog 338aa (SEQ ID NO 416)

MYFPIIVWLYVSITFVVANYGFDQWTNDDLKQFLKERKVFNDALENPKLISLANEEAKKLEKGYK
KVTEELNNLNPDDSLNDYLNFDYLFGRKENYSIKEWIFESWPVTSLOTFITQNNIQYSKDTK
DDLINKVKDQFDSISKKNHSGSFYPGNWLYESWSENLDKDWLKSYGIEFNPSSTKDQLVEKLKEFS
YQATHSIRDSKESLFDLDFDKTIFDKKGQIEDEFFQTSYSQLEWLYLHGFIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTEKKSQPWITKGEQKSQKKKGSNLINDTFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417)

ATGAGTTCATAGATGATCTGTTTCACTTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG
ATTTTGCCGCCACTTGTACAGATGGATAGAATTGAATGCAAATTTCTGCATAAAGATTAAAGTGAAA
AACAAATTTCCGAAAAAGAAGAAAATCGAACACATTAGAAAAAGAAACGAACAAAAGAAAAAAAT
TTCAAATTTAGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACCTGATTACTT
TTTATTTATATCACCTGTCAACAACAAATTTCCAAATAAATACAACCTCAGAAAAAACACTTACTAT
CTTTTCTTAGTTTGGTTTCTATAATCTTATTAACATTTCTTGCCTTTTCATCCTTGATTATCATATT
AGATCTTATCTTTAATTTGTTTGAATAATAACCAATAATCTTCCCATTAGAACTTACAACACA
ACAACAAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTTCACTAC
TAATCGTACAATTTATCATAAATACCACTGTTGCAGTATCACCTGTGTCAGCAGTTTACCAAAAC
TGAGTTTCAGTCCATTTGATTACCCAGAATTTGTTTACAGATCATAACTCCCCTTGTAAATACAA
CTTTACCTACATTGATGAATTGAATAAAGATATTCGTCCTACTTGTGCGAATTAGTCAAGACCC
TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCGTTTTTGAATGCTCAACATTTT
GTGCTAGTGAAAACCTGTGCTGTTGAAATATTGGAAGATTTCAATTGGAGTCAAGTCACCAATGAAA
GTTTGAAACCTTCAGGATTAGGTAAGATTTCAATACCTGACAAATCATCAATTGATAATTCATTG
AAACCGAAGAAGTTCAAACCTGTGAAGATTTAGATTATAGTGAAATAGATGATGACCATCATTGTG
TTTATGTCAACTTGGTAAATAACCCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTGTATG
TTTGGAAGGCTATTTACCTGGAAAATTTGTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG
CCGCAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTTGTTAGTGGTATGCATG
CTTCAATTGTCAGTACATTTATCAAGAGAATATTTGAATTTCTGAACTGGTGAATTTTATCCTAATT
TAAAGGTGTTTATGGAAGAGTAGGTATGCATAATGACAGATTATCTAATATTTATTTCAATTATG

CCTTAGTGTCCCAAGCTATAGTTAAATTGAGTGAAATTTTACCATTGAGAGAGTTCATTCAACTGG
GGTATGATGACATTACTCCAGCTCAAAAGCAACATTTATTGGCTAATAATGATGTGCAATCAGTCG
AAGTTTATGATCGTTTGTGTTAGATGACATTATTCCTAGTTTGGGAAGCAAATGTTGTGTTTAATA
CTTCCAACCTTGTTTGATAATAGCAATTTGAGGGATGAATTTAGATCAAGATTTAGAAACATTTCG
CCATTATGGATTGTGTTGGTTGTGATAGATGCAGAATGTGGGGGAAAATCCAAACCATTGGTTATG
GTACCGCTCTCAAGATTTTATTTGAAGATGACAACATGATAATCACAATTTGAAATTTAGAAGAA
TTGAAATTTGTTGCCTTGATTAACTTTTGATCGTTTATCTAAATCTATTGAAAGTATTAATATGT
TTAAAGAAATGTATTTGCAACACCTTAAAGATATTGCTGAAGGATTAACCCACCTGGTGTTCAG
ACAAAATACAAAACAACAAACCAGGTAACGGATTTGCCTTCCCATTGTTAGTCCATTACCTCAGA
AAAAACCTGACCAAACCAACACCCCAAAAATCAACAACAAAAACAACCTCAAGAACTGACAAAA
AAAGACTTACATTAGAAGAAATTGCCACACAAAACCTGAAGATCGAAGTTTATTGAAGACTTCA
GATTATCCTTTGATGAAGTTTGGCAAGCATTAAGATTTGTTTAACTAGTTATCAAAGATTCCAG
CCGTATTGAGTAGATTACATTGGTTCAATTGAATGAATGGTGGGAATAAATTGCTTGGTAAACCAA
CAGTTTATGATTACCAAAGTTCTTTTGATGTTGATGCCCTACAATACAGTCAAGTCCTTGGATAA

YML130C_homolog 580aa (SEQ ID NO 418)

MKIFRLFSLIVQFIINTTVAVSPVSAVLPKSSFSPFDSPEFCSQIITPTCNTTFTYIDELNKDIR
PYLSELVKSIFYRFKVNLDKQCRFVNAQHFCAENCAVEILEDNFWSQVTNESLKPSGLGKISLP
DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCYVNLVNNPERFTGYGNGQSFVWKAIIYSENCFPN
TNPMSVTNDADNGGEQCIEKNLFYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
RLSNIFYNYALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLLANNDVESVEVYDRLLDDIIP
SLEANVVFNSTNLFDNSNLRDEFRRFRNISAIMDCVGCDCRCRMWGKIQTIGYGTALKILFEDDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEMYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA
FPFVSPLPQKQPDQNTNPKNQKQKQPDQETDKRLTLEEIAHTKPEDRTFIEDFRLSFDEVWQALRF
VLTSYQRFPAVLSRFTLVQLNEWWNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq:
508..667; CDS: 501..1001 (SEQ ID NO 419)

TGTGAAAAAAATTTGTGGTGTGGATGTTGTTGTCGTTGTTGCGTTGTCCACAACAAAAACAAGT
AACAAATTCAAAGTTGGGCTTGGAGATCGATTTTTTTTTCCCGCGTCTGTGTGGCAGGACAAATG
AGTCGACCAGTACGTTTAAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACATTCACCTT
ATTCTATATCAATGTAAAGTCATTTTTTGATAATATCGTAATTTACACATTTTCGTATATCTCGGCA
ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTATTATCAAATCAGGAGTATAGAA
TTCCACCCAACAACCTAGATTTTCCGAATGCCAAACGACGAGGACGACACACAACGACTAAAGAAG
AAGAAGAAAAAAATATAAATAAATTGATCACGCACACATTAGAAACACAATAATTGGATCACTTTT
TTCGATAATACTACCACCACACAGCTCATTCACTCATGCCCCGAAGTTCTACTGCTCAAAAGC
GTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA
GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATACTCCATATGCAATG
GAGTATCCCCAGCAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG
ATCCACCATTTGTTACATCCAAATATTTATGCTGATGGAACCGTTTGTATTTCGATTTTACATCCTC
CTGGTGAAGATCCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAAGTATTGAAA
AGATCTTGTGAGTGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG
CTTGTAATTTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT
CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420)

MPRSSTAQKRLLEFYQQLSRDPPPGIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAVLTFPKDY
PLSPPTLKFDPPLLHPNIYADGTVCISILHPPGEDPNQYERPEERWSPVQSIKILLSVMSMLAEP
NPESGANIDACKLWRDNRAEYDRQIRQHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID
NO 421)

CTACACAAAGCTTCGAGAGTTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
CGATTGCTTTTCTTTATGATTGTTCTTTAACGGAATTGTGTTCTTTAAACAAAATCAGTTCTGC
ACGTGATATAATCTCCTATCGTAGTAAGTTTAAATTTTTTTGATCAAAAGTACACTCATCAG
TCTATTGTCGTAGATTTTCGCATACTTGTGATAATATCTGGTGTGTACACTACTTTTTTGGTTTGTGA

TTGTAAATTACAATTTTTCTATTGGTTAAATGATAATTGTTAAACAAGTCTTTTTTTTCCCGGGA
TTGAATCCGGAACTACCATTAATTCATCTACTCTACTCACCTTACACCCCTACTCACTCAA
ACAATTATATCAACCCAAAAAATAATCTTCACTACACCAATAACAAAGAACCAATAGTTCAAT
CTAATAAACCATCCTTCCCCCTAGCCTGCCACAACAACATGATTTCTCGTATTGGATTATTGAAAA
GACCTACCGTGTCCACTTTAAACAACATATGTCAAATTACAATCGACATTAGCCCTTAAAGATACA
CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC
CTACATCACCTCATTTACAAATTTATGAACCACAATTAACCTGGATCATGTCATCATTTCCATAGAA
TCACTGGTGTGTGCTATGGCCGGTGCTTTTATGCTTTAACTTGTGGATTGCTGCTACTTCAATTT
TAAATATTCATTTGATACTACTACTTTAGTATCTGCATTACCACATTACCAACATTTGCTCAAT
ATGGTATCAAAGCTATTTGTGCTTATCCATTTGTTTATCATATTGGTAATGGGATTAGACATTTGG
TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTTTATAGAAGCTGGGTATGCTGTTTTGGCTG
CTACTGCTGTCATTGGAAGTTATTTAGCTTTCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422)

MTSRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL
TWIMSSFHRTIGVAMAGAFYALTCGFAATSILNIPFDTTTTLVSAFTTLPFAQYGIKAICAYPFVY
HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron
1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)

AAAAGCAAGAAGAGAAGGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG
TTTAGAAGTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTTAATAAT
TATTTAATCAAACCTTGGTTGTAACCTATGATTATGGTAGTGATCTAAGAACACAACCTTGCAAAGCA
ATGGTAGTTTCTTTGATTTTGTGTTTCTATTAGATTCTGTTTCTATTAGATTCCCGCTTTTTTTTT
TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTTCTTG
ATTTTCTACACTACTAGTAAAAAATTTCTTTCCGCTCACTATTACACATACACTCTTTTTTCG
CACAATTACAGTCTACCAACAGGAAAAAGAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT
TGGTCTTTTTAATACTATCAATCAACTAGAGTCACAGCATGTTAATTCCAAAAGAAGACAGAAAGA
AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAATATGGCATT
TCAAGGGATGCACGATAAGTCAAGAGTTCATGAAAAAGCACAGATTATAACAGTCGTAAAGAAAAA
TTTCACTACCAACAACAATAAGAAGATATCAAAGAGATTCAAGTAATCACTACTTACAAGAAACATA
TAACATCATGGAGAGTTAATTTGAAATACGAATGAATATACAAATGAACTATACCCTTTTTATGG
CCATATCAGCTTTTCAAGAAATATTTAAACAAAAATAAATGAAGAATAAAACTTGGATATACTAAC
ACATGTATTATAGAGGGTGTCTGTTGTGCTAAGAAAGACTTCAACCAACCAAGCAGATGAAATT
GATACTAGAACTTGTTCGTATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT
CAATTCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATCTTTGAGAACCGAA
TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA
CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKKIHQYLFQEGVVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTFQFSWQYYYY
TLTDEGVEFLRTELNIPEGILPLTRLKNAPAERPRPSRGGPRRGYRGRARD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATTCTGGCACAACAAATACTTTTAGGTTACTAACATTATTTTTCTTCAGCTA
ACTAATTATCTAGTTTATATCTATATCCATTATTGTTGAAATCACTATCGTGAGGTAAATAACAAC
TACAGAGTTGTACAGTATCCAAAAAACTTTGTACCTATCAATACATTTTAAAGCAATAGGTCAAT
TTATTGCTGTAATCAAGTGTTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAACATGAAC
TATATCAACTTTAAATGCCCTAATCACGTGATACAGCACATGGGAATTTGCTGATCTTGCTTCCT
TGCACGTACACGGCACATGTACAGCACTTTTTTTTTCTAAATATTTTTTTTTTTGTTGTTGTTGTTA
TTAAACAATATTTTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCCCTTTGCATATT
TTTTTTTTTTCTTTTTCTGCCAACTTGATCAAATTCGATGCTACATCCTAATAATTCAAGTAGTCG
ATATGCTAGCACTGGAAACATGAATGAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAGA
AAATATCAAAACAGAATTCAACCAAAACCGATTTTTTTTGCTGCACGATTGGCTAGTGCGGTTGACG
ATATAGAAAGCAGTGATAGTGATGAAACGTTTATATATGAGAATAATGATACTGAACCTTGATGATA

ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA
GTGTTAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGACTGGTCCTCCCGGAACATCGATAG
CGTTAGGATCGGGCCTTCGATCGCCATCCATAGAGGGGGAACAGCTTCAATATTTTCATGACC
CAGTGAGGCAACAACAGTTCAAACTTCCTTCTACCAAGGCTCCGTCAATTTCCAACCTCCATCAGCA
GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTCAG
TGAATGATAATGACCACCGAAATCTTGTGCTACCAAACCTCAACTGAAAGGTTTACTGCTTCACCTT
CGAACAATATTGGTAATGAAAAATATACCTCAATACCAGAAAACCTAGTAGTGTGCCCACCTCAATCA
ATGAAGGATACAATGATGATACATTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT
CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTCGA
GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACCTACATACTCTGTCTC
CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACGCGTCTAAAA
GAAATTACAAAACCTCATCCACTTCCTCAAATTAAGATCAACTACATCAAAAACCTTTTCGATAAAAA
AAGGGTCACAACCAAGAAGATACAGTACCATTCTGTATGATATTGACATTGAAGATTTTCGATGATG
AGCTTATATACTATGACAACACAGCTAGGTTCCAGCGAACGAATCAACTTCATTACTAAATCAAAA
ACCAAAGAATCCCCATTATAGATCACTTAATTTGAATTTCCCTCAGGTGAAGCGCCAAAGCAAGC
GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGTATCGTGGCTCTAACAAAGATGGTACTGATA
ATGGAACAACAGTGAATCACAATATTAATTCCTTTGACTGCTAATAATAATAATAAACGTCA
ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACACATTGCTAATAATAGAG
CATTTCCATTTTCCTTATCAAGATCAACAACATCATTATTACTACGACTACGATGATTTTGACAAAG
AATCACAATCAATGGACCAATTTTGATTGGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA
ATTTTAACAACAACAATAACCCCAAAGATTTGGCGACAGTCATTTTTTCTACCAAGAAAGACAG
ATCAGTATAGTCAAAGAACAAGCTTTCTAAAGTCATGCATTTATACCTTTGTTTTGTATATTAATTG
TGCTTACCATAGGGTTTGTATTGGGGTTTGTTTTGGCCACAACAAAAGATTTAACTGATGTAGGTA
TCACATCCATTGAGAACCCCATTTAGTAAAGATGAGTTAGTTTTCAATGTTGTTATTGAAGCAT
TTAATCCAGGGTGGTTTTCCGTTGACATCAATGAAGTAGAGTTGGATTATTTGCAAGAAGTGGCT
ATCTACCTGATACAGATAATCTGAAAAATATCAACATGCGGAGGGTCACAAAAAGTAGAGACGGTTA
AATTAGGAACGATTTTGAATTTTGAATCGGTTCTCAATTTCAAAGGTGGGTTTCTCTCTCGAGAAC
CGACAATTCAAAAGGGAGGAATCCGATTATTATATCTGGCAAAAATGTTACTGCCGAGGCTAAAT
TGGTTGTAAATATGGCTGATATTAAAAATAGCTGCTTCCAATAGCATTGCTAAAGAAAGCACTACTA
GTAATGACACCAACGATAATGACAACTCCAAGAAGTGGGAAATCATATCAAGCAATCCATTTGATT
TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTCAAGAACCTCAAGATCAGTCGTGGTTA
GAAAACTGGGTATATTGATCCTACCTTATTCGTAATACCACAAGGAGAGAATAATATTTCAATTT
AG

YNL054W_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNMNTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY
ENNDTELDNANINNNNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSLRSPSILE
GEQLQYFHDVVRQQQKLPSTKAPSISSNSSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTSSQQQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKL
STTSKLFDDKKGSQPRRYSTIPDDIDIEDFDELIYDNTARFPANESTSLLNQNRIPHYRSLNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTONGNNSDHNINSPLTANNNNNNVNHDHGDNKKSN
NNNNIANNRAPFPYQDQQHYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFVLATTKDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPWFVSDINEVELDLFARSGYLPDTONSKI SNMGGSQKVEVTKLGTILNFESVLN
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVNMADIKIAASNSTAKESTTSNDTNDNDNSKKW
EIISSNPFDLIITGVLYDLPPSRTSRSVVVRKTGYIDPTLFVIPQGENNIS

YNL075W_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;

CDS: 501..1349 (SEQ ID NO 427)

CCCACAGACCAATAACGTTTTACCAACCAAACCTCTGATATCAATGATTCGAAAAGATTCAATCA
ACCCCGGTTAGCTGTTTGAGTATTGGATAGCAACACTTTCAATTAGTGCAACACAATCAAATTACC
AATACTTGTTTACCTTTTCATCTGATTCTAATTGGTTTCATAGCAATATAGTCTCTTCTGTTGTTGA
TATTAATATAAATAAACTTATTTATCAGCTGTTTGTAGTAGTCTCGCAAATTTGAAACCATGGATG
AGTAAACTTGTGTGTGTAGATGAGCTCAAATATCTGGTGGAACAATTTGTGTAGTAGTCTTGATA
AATATCCAAGAACAGTCGTGCAAGTTTCAAATACCATCGCAAAAAATCCTAACAAAAAATAAAT

TAATAAAGAAAAGAAATAATTCTATAATAGCTCATCACAACAATTCGTCTACACTTCCCACCTGAT
TTGTTGGTTTTAAATATAATAAGACAAACCTCAGAAGCTATGATAAGAAAACAGGCTAGAGAAAGAA
GAGAGTATCTTTATAGAAAGGCTTTACAGCTTCAGGAATCTTCCTTAACAGAAAAAGACAACAAT
TGAAAGCAGCTCTAGCAAGTGGAATCATTATCAAAGGAGCTTGCCGAAGATGAAAAATTACAAC
GTGATTTTATTTACGATGAAAGTGAACAAATAGAAATTGATGACGAATACAGTCGGTTGTCTGGGAA
TATCTGATCCAAAAGTTGTTATTACCACATCCCGTGATCCATCTGTCAAGTTGCTACAATTCCTGA
AAGAAATCAAGTTAATGTTTCCAAATAGCTTGAAGTTGAATCGAGGAACTATATAATCTCAGATT
TGGTAAGTACCTGTAATAGAGTGCAAGTTTCCGATATGATTTTATTTGCACGAGCATCGTGGTGTCC
CATCAAGTTTAACTGTAAGCCACTTTCCTCATGGCCCACTGCGATTTTTCACGTTACATAATGTCA
AACTAAGACACGATTTGCCAAACTTGGGAAACGCTCAGAGTCCTATCCTCACTTAATATTTGAGA
ATTTCCAATCCGACTTGGGTAAAGCGTGTGGTTAAATATTTGCAACATTTGTTTCCCTCCAGGTGTCA
AGAAAGATAGCTCCAGAGTAATAACATTTGTCAATAACGATGACTACATATCGGTGAGACACCATG
TTTACGTCAAAACTAAGGATTCAGTGGAGTTGAGTGAGATTGGCCACGTTTCGAAATGAGATTGT
ATGAAATCAGACTAGGATTACCTGACAACAAAGATGCTGATGTCGAGTGGCAGATGAGAAGATTCA
TAAGAACAGCTAATAGAAAGAATTACTTGTAA

YNL075W_homolog 283aa (SEQ ID NO 428)

MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKLSKELAEDEKLQRDFIYDESEQIEI
DDEYSRLSGISDPKVITTSRDPVSKLLQFSKEIKLMFPNSLKLNRGNYII SDLVSTCNRVQVSDM
ILLHEHRGVPSLTVSHFPHGPTAIFTLHNVKL RHDLPNLGNVSESYPHLIFENFQSDLGKRVVKI
LQHLFP PGVKDSSRVITFVNDDYISVRHHVYVKT KDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWQMRRFIRTANRKNYL

YNL096C_YOR096W_homolog 1061bp public: 1..1061; CDS: 501..1058
(SEQ ID NO 429)

TCCTTTTGTTTTTATTTTGTCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT
GACTAATATGAGATGATCGTATGTGGGTGGGTGGGAGGAAGGGACCCGGAATTC TAGGAACAGGA
AAAATAAAAACGAATAAAACAAAAACCCCCAATCGGCATGCATCGGAATTC TTTTCAGCCCAATTAC
TTTATTTTGGCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTAGCCCTTTATA
TGCAGTCTATTTTATTTTCTCTTTTTTTTTTGGCTGTTGGTAAACTTTTTTTTTTTTCGCAGGTG
TTGAAAAAAAATCATTTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTGTA
GTGAGAGTTACTCGTTCACAATAGTATACTTTACAGGGGAGTTCTTTCTTTTGGAATAGTCAACC
AACGCCAATAGCCAAGGATCAAGCTTCATCTTAATCATGTCTCTAAGATCTTATAGTCAAGAACCC
CAACTGAATTAGAATTAAGAGTTGCTCAAGCTTTCGTTGATTTGGAATCTCAAGCTGATTTAAAG
CTGAATTGAGACCATTACAATTCAAATCTATCAAAGAAATTGATGTTAATGGAGGTAAAAAGCTT
TAGCTGTTTTCTGTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAAC TAGATTAACTAGAG
AATTAGAAAAAAATTTCCAGATAGACATGTTGTCTTTTAGCTGAAAGAAGAATCTTACCAAAAC
CAGCTAGAAAAGCTAGAAAACAACAAAAAGACCAAGATCAAGAACTTTGACTGCTGTTTCATGATA
AAATTTTGGAGATTTAGTTTCCCAACTGAAATCATTGGTAAAAGAGTTAGATACTTGGTTGGTG
GTAACAAAATCCAAAAGTCTTGTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT
CTTTCCAACAATTGTACTCAAAATTGACTGGTAAACAAGTTGTTTTTGAAATCCCAGGTGAATCTC
ATTAG

YNL096C_YOR096W_homolog 186aa (SEQ ID NO 430)

MSSKILSENPTLELEKVAQAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVVF LAERRILPKPARKARKQQRPRSRTLTAVHDKILEDLVFPTEII
GKRVRYLVGGNKIQKVL LSKDSTAVDYKLDSFQQLYSKLTGKQVVF EIPGESH

YNL178W_homolog 1256bp public: 1..1024, PathoSeq: 1025..1256; CDS:
501..1253 (SEQ ID NO 431)

TGTTTTGTGTTTTGCAATCAACATAATAGAAGACCAACAAATAATTTCTATTTTTTTT GACTCTCC
CGTAGTTTACACTTCTAGCCTCTCTTGTAATATACACCTAATTGACAGTACCATTAGGACCCCA
TCTTATTGTTAAGGATAATACTTCTTCTTCTTCTTCTTCTTGTGTTAATCAAATTTGCAATAAATA
AAAAAAAACCAAGCCGACAAAGTTTCCATAAATGACTTATTTGTGTTAACGCATTAC
GTGATCATAATTTTTTTTAAATTCAAAACTGAAACCAATTCCTGCATATTGAGGTTGAAAAAAA
AGAAAAAGAAAATTTTTTCAATCTTGTGTTGAGGAGAGAGAGGTGAAAAATTTTCTCTCTCTCTT

CTTTCTTTCATTCTCATATACCATAAACTTAAACAACCTTCTTTTACTTTTTCCTTTCTTTTCCCTTT
CAAACCTCTACAACAGATCCAATTAATTAACAAAAAATGGTTAACGCTATCTTATCTAAGAAAA
AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTG
AACAAAGGTTATGCTGGTGTGAAGTTAGAAAACTCCATCTAAATTGGAAGTTATTGTTAAAGCTT
CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGAATCCATGAATTAACCTCATTGATTGTTA
AAAGATTCAAATTATCTCCAGAAGGTATTGCCATTTATGCTGAAAGAGTTGAAGAAAGAGGTTTAT
CTGCTGCTGTTCAAGCTGAAGCTTTGAAAGCCAAATTATTGCTGTTTACCAATTAGAAGAGCTG
CTTATGGTGTTTTAAGATTGCTATGGGTGCCGGTGCTAAAGGTGTTGAAGTTGTTATCTCTGGTA
AATTAAGAGCTGCTAGAGCTAAATCTCAAAAATATGCTGATGGT'TTATGATTTCATTCTGGTCAAC
CAACTAGAGATTTTCAATTGATATTGCCATTAGACATGTTTAAATGAGACAAGGTGTTTGGGTATCA
AAGTTAAATTAAGATCCAGCTGCTAATAGATTGTTGTTCCAAGAGCTTTACCAGATTCTGTTA
AAATTGCTGAAGCTAAAGATGAAGATGAAGTTATTCCAGCTCCAAGTGTAAATCTTATAAAACAAA
CTGCTGAAGATGAACTGAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT
AA

YNL178W_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKKLVDGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLGEOGRR
IHELTSLVKRFKLSPEGIAIYAERVEERGLSAAVQAEALKAKLLSGLPIRRAAYGVLRFAMGAGA
KGEVVI SGKLRAARAKS QKYADGFMIHSGQPTRDFIDIAIRHVLMRQGVLG IKVKIMKDPANRF
GPRALPDAVKIAEAKDEDEVIPAPTVKSYKQTAEDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:
501..2102 (SEQ ID NO 433)

AAACTTTCTGATTGAATAAAGTGAACCTCAAATCACATTCTTCGGCATATATCAAACCATTATTAGT
TTTATCAGCTAAATCTTCAATATACTCAGCCACCCATTGATCATTGGTTCTTCTAGTAAGTAATAT
TAGTTGTGCTCCTCGTTGTGCCAATTCATATGCTATTGAGCTCCAATACCAGTGGTCCCACAGT
AATCATAAACACTTTCCCATGCATGTCTCGCTCCACGCTATTGGTGGCACCATGGAAATAATACTT
GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTCTTTAATTTGGTCCCAATA
TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATTCAGTGGCATAATTGGTATATC
AAGAGTGAAGAAAAATGCTGTATTGGAGGTTGGAATTTGTTTCAAAATTTGGTTGCCTTTTTATTTCT
TCTTGTCTTTTTTTTTTTTTCAGTGCTAACATAATTTGGGATGTATGTATTGAAAAAATTTTG
TACAATTTCTTGTCTTGTCTCCCACTCATCTCGCTCTCTTATAAATTCACAAACATGGATG
AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATTCATATGGATATG
TTACATCAATCCATTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA
CTGCCATAACTGGTATTGGCCAGGAGAAAGAATTTTCACTGCTGTTCTTAACAAGGCATTAATCA
ATGTATATTCATGGGGAAGAAAGTGTGATCAACGTATACCGATACCAGAAGCATTGACTTGTA
TCACGTTGATAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAGTTATACA
AATTACCAAATTACCGAGTTCCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTTGACATTT
GGGAATTAAGTTCAGGCAATTTATTATGTGTCAGAGACGCCCATTTATCAGGGGATCACTACCATCA
AGGGTTCAAGCTGTGGAACATTTTTAATTACTGGAGGAGAGGATGCCAGATGTCTTGTATGGAATT
TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAACCATATTGGCAAATCACTG
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAATTAT
ATACAACCTTCAGAAGACAGCAGGTCAGGATTTATGATATAGTCACAAAGAGTTTGTAAACCACAT
TTATTTTACCCAGTTCGCTGAATGTATCACCAGGATCCAGCTAATAGAGCGTTATATGTCGGGT
TGAATAACGGTCTTGTAAGATCAATTCCTTTATATTTCTATAAATAGCCATACATCAGTGTGGAAA
GTATTTGGCGGCATGAATAAGATAATCAGGTTGATGCTGATCAAAATTTAAAGAGACATTTGTTG
CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTGTTACGAAATTTGACAATTTCTT
TTGATGGTACAAGTATAATATCTGGTGATTCTGAAGGCAGAGTGTTTGTGTCTGACATTGTAACGA
AACAAGTTGTGAAATCATTCACACCTTGTAACCTCCAATAGCTTATATTGCTGTTGAAACTATCC
CTGATGACTTTGTCAATAACTTAGCTACTAGTACTACCCTAATAAAGCTGACAAGAAACATAGAA
TGATACCTCAATTTAAACGAGTACTAGCAAGCACCATTCTGAAGAACATCAGATATTCTTGGACA
TTCTCTGGTAAAAACCACGCAACCACCAACGCAACCGGCAATATTGACTTTGCAACTTGGTTACAAG
GCAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAACTCTATTGTCAAACAAGTTG
GCAACGGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTA
GAAACAAACATGAAGAATTAATTAAGAACATGCCAAATTTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)

MYVLKKKNFVQFLVLVPLISSLSYKFTNMDEVVFYIAQGD PADKHSQESYGYVTSIHSSKQYASY
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALTCITLINHPNGSNNN
SDNDDNQLYKLPNYRVPWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTITKSSCGTFLITGG
EDARCLVWNLAELISIDYKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSEDSTVRIYD
IVTKSLLTTFILPSSAECITKDPANRALYVGLNNGLVRSIPLYINSHTSVLESIGGMNKIITVDA
DQNLKETFVAHQQKTKTGDDKPVVVKLTISFDGTSIISGDSEGRVFSVDIVTKQVVKSFPTPCNSP
IAYIAVETIPDDFVNMLATSTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG
NIDFATWLQKGQSEELQFKNLSGINSIVKQVGNENVSDLEERLQRVSQAYTEL RNKHEELIKEHAK
LLDKLE

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

TTTCTGCAAGTATTGCGTGTGCTGCACAACTTTTTATATCCGAAAATTTTGGCCGGGAACGAAA
CGGCAAGAAAAAACAGAAACAATACCACCAGCACGGACAAAAAGATTATAAGCTTTGTGTAATAAG
GTTATGTCATCGGGTATTACAGATTGCAGGGCCATCTTGCTTCATCAGTTATAGCATTTCAATAA
AAATAAGCCACATATGTGTACAGCGCTGAGTCTACTCAACATGTGTAAATAGAATAAATCAATTGA
CACAGTCTTTTGAGATCTGTTATTCTGGCCTATAGCGTTT TAGGAAATTGCGGTATTTTCTGTCT
GTTTTTCTTTTATCTATTTTTCGCACGACTTGGGGTGGTTTGTGTGACTTTTTTAGCAAATTAATTT
TGTCGGTCTTCGCAGTAAAAATAAAAAATTCAAAAAAACAATTTGACTTTTTTTTTTACTTTT
CTTTCTTTTCTATCAACAATACTAATCACAAGCCAACCATGAAATTCACTACTGTTGCCACTGTTT
TTGCTATTTTCTCATAGCTGCCGCTAAAGGTGGTGAAAAAGATCACGGTAAAGCTTCTACTGTCA
CCAAATATGTCACTGAAACTACCCACAGATACGGTCGTTTGTACAAAACAGTAGATCTAAAAAGC
CAAAGGAAACTGGTACTCACAGATACGGTAAATTCACAAGACTCCACGTCCAGTTACCACAAC TG
TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAGAGATGCTGTTGTTGCTAGAGATTCTAAAAACG
CTTCTTCCAACTCTACCACCTCTAGTGGAACAATGGTGTCGCCACTGGTGTCAGCTTGGGTCTTG
CTGGTGTCTTAGCTGTTGGTGCTGCTTTGGTCATCTAA

YNL190W_homolog 131aa (SEQ ID NO 436)

MKFTTVATVFAISSLAAAKGGEKDHGKASTVTKYVTE TTHRYGRFDKTSRSKKPKETGTHRYGKFN
KTPRPVTTTTLVKESDLPKKRDAVVARD SKNASSNSTSSGNNGVATGVSLGLAGVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCCTTTGTTTTTTTTTTTTGGGTGGTGCTGTGGTTCGTTGGGTAGTTGGCTCTTG
TTTCGGTTCTACTTGTTCCTTTTTTTTATTCTCCTCGTTAATCCTAATTTTGTGTAACAAATTAAT
TATAGGGAGTTGGAAAATTTAAAGCTTGAAAAGAAAAGAAAAGAAATACCAACGTGGAATTTCT
ATTACGTAAGTCACTATAACTTGCATAGAAATTT CAGGTTTTCAATTTAAGAAAGTATTAATCAAC
TGAATTAAGCAATTGAAACGAATTGAACCAGCTCAGCATTTATTTTTCGTTTTCTTTTTTTTCAA
GGGGGTGGGTGAAAAGAAAAATCTAAAAATATATAAATACTCCACTTATCTCCTCTCTCTCTCTCT
TCTCTCTCTAACTCAATTTCAATTTTCCCAAACCAAAATTTCCCTTTCTTTCTTTCTTTCTTTAT
TTTTACTCAATTGAATCAATATTTAAACAATAAAAGCCATGTCAGCTAACGATTTTTATTTCATCTG
GTGATCAATCCAATTATGATCCAAAAAGATCCTCGAATCAAGGATCATCATCAATGATGAAC
AACAAGACAGAGGGTTATTATCTACTGTGCGCGGTGGTGTTGCTGGTGGTTATGGTGGTCACAAAT
TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG
CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACAGAGCAACAATATGGTG
GTAGTGGTAAACACGAAGGCGGAAGACATGAAGGTGGTTTTGGTGGTGGTAGACCAGATGATCGTT
ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG
GTGGTGGTTACGGTGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTCGGCGGTGGCAGAC
CAGATGACCGTTTTGGTGGCGGTAGACCAGATGACCGTTTTGGAGGTGACAGAAGAGATGATAGAA
GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)

MSANDFYSSGDQSNYDPKRSSNQSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGT LGTV
LGAIGGAIGANKLEDAYEDRKEHKKHEQQYCGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG
YNDRRDDGYGGGYGGGRPDDRRHEGGFGGGRPDDRFGGGRPDDRFGGDRRDDRDRRDRW

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTGAAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG
TTTGAGGGGATGTTTCATTAGCAATGTATATAATTATTGTATATTATGACAAAAGAAAAGAAAAAGAA
AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAAATATCGCTTATATTGTGATAAAAAATT
TGAAAGACAATCCGAATGTAGTGCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT
TGAGGAAATTCAGATAGCTAACGGTTTTGCGATTACGAAATTCGCAACCAAATAAATATGTGACA
AGGAATACACTACTGATCAAGGTATTCTTAGTACAATGGAAAAAAAAAAAAAGAAGCAAAACAAAA
AAACGAGAAAATTAATGAACACGACTTCACTTCTACAACCTACTGGGAAAAAAAAAGGCAGAGAGTTA
TTGAAAAAGGATCATATCAAGTTCTTATTGTATATTATATGAAGTTTTCTGTTTTAGTATTACTTG
CCAGTTACTTAGTTGGTGTGAATTCTCTGATTGTTGATACTTCAGAGGAATTAATTTGTCCAGATC
CAGAAAACCTTTAGATTGTTATCCAAAATTGTTTGTTCACAAACGAGTGGCAAACCATTAAC
CAGGTCAAGATATACCACCTGGGTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA
AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG
ATCATTGAGGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA
AACAGGAGCACGCTCATCGTACAAAGGTTAGCCAGGGAGATTGAGTAATTTTGACGCAGCTTGTCT
TGGAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAGGTTGCATTTGGCACTAGATACTT
TAGAGGAATTAAATCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAAGCCATATTTCAGA
GTTTTGTCAACATTGCCAATGGTGCTTCTGATCCAAAAATAACCGAAAAGGTATATCGTGTAATGG
GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG
TGGATAATTTGTTTGAGCAATTAGCGAATGAAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA
TTCAAGCTTTAGTCCAAAATAGCCATTTTGCAAGACAATATTTTTCATTTGACCACAGTTCCGGGT
TAAATGATTTAATAGCGATTTTTCCTCAAACTTGGTCCAACTCAAAGTCCAGGGCAAGTAACATTT
TAGAGGATTTACAATTGTTCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT
CACAGGTTTCAAAATTTATTTCAGAATTCCTTTGTGGAAATAAACTTGACGAGAAGAATTTCAAGT
CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTTCGACCAAGTGGTGACTTTC
TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAGAGACGATTATTCACAAG
AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT
TAAGAAAAGCAATTGCCGACGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASVLGVNNSIVDTSEELICPDPENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVR
NIDTLEKEAKLMSADEKDEPVQEVVVGELQDHSREAITENLQKLHESKHPEVKQEHHRKTKVSQ
DLNFDAAACSEIESFKPHESDVERLHLALDTLEELSHDIEFGVKLTSDKAIFQSFVNIANGASDPK
ITEKVYRVMGSSLRNNPEAISNILTDFDKSYVDNLFEQLANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRSLEDQDPESQVSKFIQNSFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEVESRKENKKRDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADL

YOL048C_homolog 1244bp PathoSeq: 1..27/985..993, public: 28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTTCCTTGATTTTAGAGCTGTTAATTATACCTTTTTTGTTCCTCAATAAGCGCTAAAAA
TGATTGAAATTAATAATACTAATACTATTCCAGGTCAAAGTAAACACTATAAAACAATATATTTCAAT
AACAGGAGCAGTAATTAGCTTCAACATCAAGGTACTCTTTTATTTTTCTACCAAAAACACATCTGA
AGTAGCTCTTATCCATAGATCCAAATATTTAACCTTTTTTTTTTCTACTCTCATCTACTTTTTT
TTGCAACACTTACTGCTCACAAACGCAATGACCATTAATTTCAATAATCAAATCAAGAGCT
TATTTGTATCCTCTCAAGGTATGTTAATGTATTAACAACACCGATTCTATTTACCAACTAACACG
ACAGAAAGGGGTTGTACTATTTGTAACACATCCACCGTTTGGCCCTTTTACATAACCATATTGA
TACCTCAATTGGTTCCTTACACTAGTCATTTACCTGATTATGTTTTATTGTTCTTCCACCTCAAG
CTATTGTATATACATTGTTAATGGGACCATTAGGGGTGATTGGTGCCTGGTATAGTTTGATCCTGC
AAGCGAGCACATTGTCTATATTTGTTGTCACAATATCCTTAATGCCTCACATACAACGAGTGGCAT
ATGATGCAATATTGAGTAGAGAGTGTGCAATGATGTGGTACTAATGGGAAACTTAGGAGGTATA
GAAACTACCCATTAGAGTAAGGGCCAGAGAATACCTTAAGGCCATTCCAGATTTTCGATCTTTT
CCTTCTCTTTGCTCAAGCTACTTGTGTTTTTCGGTATTTACTTCATACCTTTGTAGGTCCAATCA

TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG
GGTTTCTGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG
TGGTTGCGCTTTGGCTCGAGCTGTTTCCATTTATCAATATGTTTTTTATGTTCCACCAATACTTTGG
GAGCTGCTTTGTGGGCAGTTGATATTGAACAACAAGAGAAGGCCGTACAGAGAATGTGGCCGCAG
CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG
AACCAGCAACTAATATACCTGAGGCTACCCCAAAAACCTGCTACAAATACCATCTAA

YOL048C_homolog 247aa (SEQ ID NO 442)

MFSLFFPPQAIVYTLLMGPLGVIGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRECANDV
VLMGKLRRYRKLPIRVRRAREYLKAIPDFSIFPFLKLLVFFGIYFIPFVGPIIVLFFQSSKRLK
AHARYFKLGFSRSDIRTIHKLNRPAYMGVGVVALWLESFPFINMFMFTNTLGAALWAVDIEQQE
KAVTENVAATTTATDTNSVNQQGLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public:

948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)

GCATTTTACTTATTTAGATATTACTTCATATTGCTTTTATTTAGATTGATTTTGTTTAACAGTGAA
AGTTTTTATTTTTTTTTTGTTTAAAGTTTTTATTTTTTTTTTGTTTAAAGTTTTTGTATTATACAA
TATTTAAATTATAGTAATCATCTATAAATTTCAAAGTCAAAAGACAGATCTTAAGGCTTAATTAA
TAACTCTCTATGGCCTTCTGTGTCAAATTTGTGTCGTTTGATAACAAGTTTGGAAACGGTAATGGTT
GAAATTAGAAAAGAAAAAATTACACATGGTAGCAGCTGATGTATAGAACTTCTAGCAAAAAAAA
AAAGAAAGAATTTTTTTTTTCTTCCATTTTCAAATTTGAGAGATCGAAATAATTTCTTGAATTTA
TTAAAAGGGAACCCCTTCCCGAAAAATCCAAAACCAAACCTCCACCCAAATATCAAATAACTAAC
TTATCATTTCCAACAGATAATATTCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG
AAGGTAACAAATATTTTGCTGCTAAAGATTTTGAAGGCGATTGAAGCATTCACTAAAGCAATTG
AAGCATCACCTGAACCAAACCATGTTCTTATTCTGTTCTGGATCTTATGCCTCTTTAAAG
ATTTTAACAACGCATTAAAGATGCTCAAGAAATGTGTCAAGATCAATCCTAGTTGGGCCAAAGGGT
ATAATAGAATTGCTGGGGCTGAATTTGGTTTAGGTAATTTTGATCAAGCCAAATCCAATTATGAAA
AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAAATCAGTTGAATCTGCTT
TATCATCTGGTGGTGGTGGTATGACAAGGATTTAGGATTTGGTAAATTTTAAATGATCCTAATCTTT
ATACTAAATTGAAAAATAATCCTAAAAACAAGTGAATTTATGAATGATCCTCAATTTGTTGCTAAAC
TTGAACGTCCTTAAACTAATCCACAATTTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA
CGGCTTTTGGCTTTAATGGGTATTGACATGGATTTACCAATATGGGATTCAGTGTCCAAACG
AATCACAATCCAATGCATCAGAACCAAACTGGAACCAAAATCAGTACCAGAATCTAAACCAGAAC
CAAAAGCAGAACAAAGGAAGAAGAAATCAACCTCAGCCAAAGATGAAGACACTCCAATGACTGATG
CCCAAGACGACACTAATGATAATGATGCCAAAACCCAAGCTGACAATGCTAAAGCTGAAGGTAATG
CCTTATACAAGAACGTCAATTTGATGAAGCAATTGCCGCCTATAATAAGGCTTGGGAATTACATA
AGGATATCACTTATTTAAACAATCGTGCTGCTGCCGAATATGAAAAAGGTGATTATGATGCTGCTA
TTGCTACATGTGAAAAGGCCATTGATGAAGGTAGAGACATGAGAGCTGATTATAAATTGATTGCTA
AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAGATGAATTACCCGAAGCAGTGAAAAATT
TTGAAAAATCTTTAACTGAACATCGTACCCCTGATGTTTTTAAATAAATTAAGATCAACTCAACGTG
AAATTAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG
GTAAAGAATATTTACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA
GAGCACCAGAAGATGCTAGAGGATATTCTAATCGTGCTGCTGCATTGGCAAAATTTGTTATCATTTT
CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTCAATTAGAGCTTATATTA
GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTCATGGATACTTTAACCGAGGCAA
GAACTAAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAAGCTA
CTTATCAAAGATTTCAAGCCATTGAAGGTGAAACTCCTGAACAAACTATGGAAAGAGTTTCTAAAG
ATCCAGAAATTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA
ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG
CTGCTGGTGTATTTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)

MTADEYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLYSNRSGSYASLKDFNNALKDAQECV
KINPSWAKGYNRIAGAEFGLGNFDQAKSNYEKCLELDPNNAMAKEGLKSVESALSSGGDDKDLGF
GKILNDPNLYTKLKNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTAFALMGIDMDL
PNMGFTAPNESQSNASEPKSEPKSVPEKPEPKAEQKEEESTSAKDEDTPMTDAQDDTNDNDAKTQ

ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYKGDYDAAIATCEKAIDEGRD
MRADYKLIAKSFARLGNIIYLKKDELPEAVKNFEKSLTEHRTPDVLNKLRLSTQREIKTRELNAYIDP
EKAEEARLQKEYFTKGDWPNNAVKEYTEMIKRAPEDARGYSNRAAALAKLLSFPDAIQDCNKAIEK
DPNFIRAYIRKANALAMKEYSHVMDTLTEARTKDVLEGGKSIHEIDELMKNKATYQRFQAIEGETP
EQTMERVSKDPEIVQILQDPVMQGILAQARENPAALQDHMKNPEVYKKNMLIAAGVIRTR

YOR312C_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)

CCACTAACAACTTTTTTTTGGACTATACACCACTGAAAAAAAAAAAAAAAAATTTTTGTAAAAATCT
TAAGAATTTTCAGTTTAGAAGGTATTCACAACAACCGAAGAGTATGTTCAACATCGTTATAATAGA
ATAGAATAAGAGCATGACAACAAAGGGATACAAGCTTGAAAAAAGAAAAAGGGTGGGATATCTTAA
AATTATTAAAGAGTTTTTTTTTATAACATGTCATTGAGATTGAGATTGGGAATACTGAATTCGATTT
TAAAGTCATTGGATGGGAGAGTTAATTATTCGTTTTATTATTAGGATTACCAATGAATAGTAATGA
AGTGATGGAGAGATAGAATGAAAGTATTCAGAAGAGCATCAAGTCCCTTATAAGTTTGTGAGACAT
AATATGTCTACCCCTTGTCAACTTGTCAATAATTTTATTGCTCGTCCTTTAAAAGAAATGAATAA
AAAGATTTACTAACTTAATTTCAATTATTTATAGAAAGATGTCTAGATTAACGAATATCAAGTTA
TTGGTCGTAATTTACCAACTGAATCCGTTCCAGAACCAAGTTGTTTCAAGATGAGAATTTTGTCTC
CAAACACCGTTGTTGCCAAATCAAGATATTGCTATTTCTTGCAAAAATTCATATAAGTAAAGAA
CTTCTGGTGAAATTGTATCTGTCAACATTATTTCTGAAGCTAAACCAACTAAAAGTTAAAACTTTTG
GTATTTGGTTAAGATATGAATCCAGATCTGGTATTCATAACATGTACAAAGAATACAGAGATGTTA
CTAGAGTTGGTGCTGTTGAAACCATGTACCAAGATTTAGCTGCTAGACACAGAGCTAGATTTAGAA
GTATCCATATTTTGAAGTTGTTGAATTAGAAAAACTGATGATGTTAAAAGACAATACGTTAAAC
AATTTTGGACTAAAGATTTGAAATTTCCATTACCACACAGAGTCCAAAAATCTAAGAAATTGTTCC
AAGCTACTGCTCCAACCACTTTCTACTAA

YOR312C_homolog 172aa (SEQ ID NO 446)

MSRLNEYQVIGRNLPTESVPEPKLFRMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIISE
AKPTKVKTFGIWLRYESRSGIHMYKEYRDVTRVGAVETMYQDLAARHRARFRSIHILKVVELEKT
DDVKRQYVKQFLTKDLKFPLPHRVQKSKKLFQATAPTTFY

YOR369C_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS: 501..929 (SEQ ID NO 447)

TGTTTACTTTTTCTGTAGTTTTAAAGTTTCCTAATTTAACTTCCAAAAGTTTCATTAACAACAATA
TTAACATACCTTTGTCAAGCAATTATATTGAAGTTTTTTGATACAAGTGTTGTTTTTTTGTG
TACATGTGAGATATATAATTGTGTATATACAGTCACGTGAATAGAGCAGAAAAATTACGAAGTAGA
AATATTGGTAGCGCGTTAGGGCTATAGCCCTATTTAGTTTGTGCACCACACGACTTACAATTTTTT
TTTTTTTCTTTCTTAGAATCCTTGAGGCACTGACACTGTACTCTCTCTCTCTCTCTCTCTCTCG
TAGGTAGTGAAAAATTTCCACTAGTCTTCCATAAACCACCTAGGTTCTTTCTTTTGGAACCACT
GAGCAGTAAATCAATTTACTTGACGAAGAAGTCTATACATAAATATAAACTGTCCCTCCCCCCC
CTTTTTTTTAACTAACTAAGAAGAAAAAATTAAAAAATGTCTGACGTTGAACAAGAACAATTTG
TTGAAGAAGTTGTTGTTGAAGAACAATCCGGTGCCATCACCATTGAAGATGCTTTAAAAGTTGTTT
TAAGAACTTCTTTAGTCCATGATGGTTTAGCTAGAGGTTTAAGAGAAGCTTCTAAAGCTTTATCTA
AAAGAGAAGCTCAATTATGTGTTTTGTGTGACTCTGTTACTGAAGAATCAATCATCAAATTGGTTG
AAGCTTTATGTAATGAACCAGAAGAAAAATCCCATGATTAAAGTTTCCGATGCTAAATTATTGG
GTGAATGGGCTGGTTTTATGTCAATTAGATAGAGATGGTAATGCTAGAAAAGTTGTTGGTGCTCTT
GTGTTGTTGTCAAAAACGGGGTGCTGATTCTGATGAAAGAAACATCTTGTGGAACACTTTTCTC
AACAAATA

YOR369C_homolog 143aa (SEQ ID NO 448)

MSDVEQEQIVEEVVVEEQSGAITIEDALKVVLRSLVHDGLARGLREASKALSKREAQLCVLCDSV
TEESI IKLVEALCNEPEEKIPLIKVSDAKLLGEWAGLCQLDRDGNARKVVGASCVVVKNWGADSDE
RNILLEHFSQQ

YPL047W_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS: 501..878 (SEQ ID NO 449)

AAAATTTCCAATCTTGAATTTTCATCTTCAACGTCATAAACCTGTTCTGTTTGAAAATTTATCGTCCT
CATTATCGTTGTCATTTTCATTGTCAATATTACGGTTACGATTTTGTTCCTTTGAAG
TCTTTGACTCTAGCTGTTTCATCTGTCATTACCCCTGGCTTGGTTTGTCTTACTGTGAGCGATGAG
ACAAACTTTTTGATTGATTGCAACTGAACAAAAAATAACGACAGACACACACACACACAC
ACACAATTTTCAGCTCCTTCCAAGTCGTGTTTTTTTGGGAAGAAAAAACAACCTTGGCCCTAAA
AACTCTATGCTCTAACCGACAACATTAGATTACTTTGATAACTCACAACCTTTAATTAACACTATC
TACAAAAATATGACAAGTACACCAATAACGTACAAGACACTAGTATGAAAGGCAAGCACAACTTGC
AAACAAAAAACCCCTAACTTTTATTATAGTTTGTGTTGATGTTATTTGTTTTATACTAACTAAAA
TCTGTTTTTTTTTTTTTCAAAGGCCGATTCTATATTTAATGATCTAATCAACAATATCATTAAC
AACATACATTAACAGTTTAACCAATATTAAAGATCATTCCTCATTATTAAATTCATCTAATAGCA
ATACTAATAGCAATACCAACGGTACAATTGCCAGTAATGGTGGAAATGGGACTACAAGTGATGAAA
ATAATGAAATTGAAAATTCAACAATTCAAGATAAATCAAAATTAACAATTAGAACTTCAAGGT
ATTTCCGATGTCTTAATTGTGGTAGAAATATTGCCGGTGGGAAGATTTGCATCTCATATAAGTAAGT
GTTTAGAACGGAAACGGAAATGA

YPL047W_homolog 126aa (SEQ ID NO 450)

MLFCFILTKICFFFFSKADSI FNDLINNI IKQHTLTSLTNIKDHSLLNSSNSNTNSNTNGTIASN
GGNGTTSDENNEIENSTIQDKSKLKQLETSRYFRCLNCGRNIAGGRFASHISKLERKRK

YPL137C_homolog 5344bp public: 1..3342, PathoSeq: 3343..5344; CDS:
1250..5341 (SEQ ID NO 451)

CTCTAGAAGTAGGACATCGTATAGTGATAAACACTCAATAAGTAATGAAGAAACACGTTTGTG
TGCAATGTTAGCTGGCGAGCTCAATATTGGGTCTCTCCGCCGTCTGTCTGCCTTGCATTCCTACTTT
TTTTCTCCTTATGGAAACATTAGTACTAGTAGTGGTGGTAGTAGTTGCTGTTGTTTGCACCTTGC
ACGTAGTTGTTTTCCCTCATTCTTTCATCTGATTATTCTGTCTTTGTAACTGCATACAAAGGGA
GGGGAAGAAAGAAACAACAAAAGGGGAATTTGAATAGAAATGAGTCAATCTTTAATCCTACTACCACGGG
GGGGGGGGGGTCTACTTCTTGGTGTAATAATGTATGGAGATTGAGGTATTAGACTTTTAGAA
AGAGGTCTTGGTTGAGTAAGCGGGATAGCACAAATAATGCGTGTCTAATTGGTCAGAGAATAATA
TGCTTTGGGGAACAATAGAAAGATGTAGCGAGAGAAATAGAATTNCAAGGGTAAGGATGATTAAC
TTTTTTTTTTTTAATGCTTGGAGTACTTTGTGTTGGAAAGAGTATTGCAGAAAGTAATAGTTTAA
AAAAGAAAAGTATATAACTTTAGTAATCGGAGAACAAATTGAAATCAATATTTTGAAAAATATAGTTT
TATAGTAGTAACCTGGGTCGAGGTGAACCCGAATTCAATATTGGTTTTTCGGTTGTTATATGCTACAT
AACCATCCTCATCTTGAATGAAACAAGGATTAAGATAATGAGTATATTAAACAACAACATTATGT
TGTTACTGTTGTATTCTGTTTTTTGGTCATTGCCATGGTAATTTTCATATTTAGTAACAATTTAGTG
TTCATCGTAAGTCTCTCCTTCTCTGGGAGATGTTCTCTCTCTCTTCTCTCTTGTGTTGTTGT
TGTTAATTGTTAATTGTTGATTATTGATTGTTCCCAATTAAAATTCCGATAAACTTGAACAATAA
ATTGTCATCATAAATTTTTTTTTTAGAAAATCACTCCATAAATTAAATTTATTTATATATTAATTT
TAAATCGGAACCTCCGTCAATTGGATTCCGTTTTTTTTTTTTTTATTTGTTCAATTTATTTCTTGAT
TTTATTTCTTTTTTGCTTCTACTTCTCTTTATTTTCTTAGTTTCATAATTTTGACAGATAATA
CTTGAAACTGGTTAATTTTAAATCAACTTCGTGATTTTTTTTCCGGAATCTAATAATATCAATGAC
CAGTAATCTGCCACCACCTTGGTTCTACAACCTAACGATCAGAGACTACCCCAAAGCGAGTTTCATC
CATACCCAACAATAAATTGCCTTTACCTAATGCCAATGAAGATTTTGCCACGGGTGTGTCGAATGG
AGATGTTGACTGGCTATTTTCAGGTAATCAAAGAAATTGGGGAAAAAGATGGCTAACAACAATGC
CAATAAGGATGAACGAAAGAATAGTCATGGTAACATCAAAAACTCGGAAAAAACTACCGCAAAACC
CAATGAAACTAAACATGAGTCTAATGGTGAGAAGTTAGAATTCAATGTTCCAAAAATCTGTAATGCC
AACAAAGCATACATCGTCTGGGAACCCAAAAGCACCTACCAATGGACAAATCTCAAAATGTAACACC
AAGTCAACCAAGTCCGAAACAGACCACTTCTGGGTCAACAATGCAATGATATACCTCCAATTTT
TCCTAAACAACCAGAAAAGGCATCAAGTTGAAATAAACTAAAAATTTGGGCGTTCAAGATCGTCTTC
TGCATCAACAGTCGTACCTTCATCTACAACAGCTTCAACTACTACTAATCCTGGAGATCCTAAAAG
TCAACCAAAAAGACGGAGCAGTAGTTTAACTTTGTTACTCCTTCTTGGAGAGTGATTTGGCATA
TGACGATCCTGCATTGGTATCTCAATTATCAAACAATTCAAATTTCTTGAACATCATCCTCGCCTAA
TGTTTCTCGTTCAAATAGCAAAAAAGGTGGGTTATTCAAGTTCACTTTTCATCAAAAATTTAGATCAAG
CTCGGCTTCATCTAAACAACCACAACCTGCATTCATCGTCTACACCATCAACCACAACGACAAATGG
TGGCGGTAACCTCGTCCGCTGCTCCAAAATCATCCACTACTCCCCAAATTTAATCCTTCACTTGT
TGGTCCAGTATCAAAGCACAATCGAGAAGCTGAAGATTTGGTGTCTCTTACCAATATTTGCCTGC
TGGGAGTGGAATACCAATTAAACGTAAACCATCAATATCGGGAAATTCAAATTTTCAAAGATTCATT

TCTCGATGATGCAAGTTCTTCACCGTCATCTTCATTAAACTCTGATGGGGGGCTTAAGTTTTTTCAG
GAGACGTTCCCTCTGTGGCATCTACACCATCAACACACGCGTCAACACCTCGAGTGATTTTGAACAA
AAACCCCAATAGGAGAAAAGTACCCATTGAAGAAATATCTGAAGTTGCGTCGGGTTACCTT
TTCTGTTGATAAACTCGAGCAGCATCCGCAACAGCAGATTCTTCAAGAAGACCTAAACGAGGTAA
TGTTTTTAATTCACAGGACATCAATGCACCACCTCCAAGACTATGTCTTGGGATTTTCAGTTAATGA
ACCAAATAATAAAGATGACGGTAAATCACACAACCATTCCAAATATAGTGATCATGAAATTGCATT
AGCTGAAGATGCTCAACGCCGAGCAATTATTTGAAGCAGAAAAACATGCTCAAGAAGCTCATCGACA
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AGCAGTTGATAAAGAAATTGGCAAATGATGTTTTCTGTGGATGGACCGTTGCATGTCCACGAACAACA
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GAAAAACTTCTTGGATCGTTGACATATAATAAACAATTGGAAAAGTTATCGTTGAGAAATGTTTC
CATTGATGAGTTGGGATGGAAGTATTTGTGTGAATTTTTGGCAACAAATAAAACAGTTAAGAAATT
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GGATTATTTTATTCGATCATTAAATTTTGGCGTGGTGAATAGAAGAATTGGTTATCAATGGATGTAA
ACTATCCGATGCAATATTTGAAAAGTTTCATCAATCAAGCGGTTAAGAAGTCAACCTATCGATTAGG
TATTGCTGGTATTGATTTGAATGTTAAAAAATCAGAAATGGTCACATCGTGGTTAACTGATGGTAA
TTCTCAATGTGTTGGTGTGATATTGCTTTTAAATGATTTGAGCAAGGGACAATTACGTCCATTTCAT
TAATGCGTTTAAACACTGGCAAGTCAACAATTTAGTGTTTTTTTTTCATTGAATTC AACCAATTTACT
GAACATTGAAGAACTTCTGACTTGATCAAGTCATTAATTAATGTTAAAAACATTACGATTTTTTGA
TTTAAGTTCCATACCTAATATCTTCCCGAAAATAATTACCCATTTCGGACAAATACTTGGCCAGATA
TCTTAATCTTCGAAGAATACATTTTGATCTTAAATGAATTAACCGCACAAAGCTATTGGGTCATTGGC
GGGGTGTTTTACTGAAAATGCCCAATTAGTTTCATGTCTCGTTATTGGGTAATAGAATTTGTCAAC
TACGTCAGCAGCTACATTATACGGAGCAGTTAAACAATCCAAGACCTTGTTTGCTCTTGATTTGGA
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CACTTTGAAGCCATCTCATGGCGGCAATATTGAAAGCAATCCAGAAAAACCAGAGGATTTGATGTA
TGATGGATCGTTATTAATGGAACAGCTGAAAAATTATAGTTGAAATAGAAAAGGGTAAGAAAGA
GGATATCAAAATGCAAAGAATTATATCCGATTTCAGTATTGGAAGAACAAGATCGATTTCGAAGGA
TATTACAAAACCATTGATACATTATTCGAACAAAGAATTTAGGTAAATTCATTTGAAGGTAA
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GCCATCGGTCACTGTTGATACAATCCATGAAAGTGCAATGAGTTGATTACTGCTGGACCAATTTT
ATCACCACATGTCAATAGGAAAGCAGAACAAAGCTCGTATTTCCAGTGTTTGCCAAATAATGATAA
TTTGACCCCTCATCAAGTTGTCGTTGAGTCAAATGATGAAGGTAGAGATGTTCCAATAGATAAAAT
GACAGGACGACAGTTTTGTATTGATCAATTAGTCAAACCTTCTGTGCATGCAAAAGAGCAAGAAAT
TGAAGAAGGGGAGCTTCATAAATTTGGATTCTTTATTCAACAAAAAGAGAGACAAAAACAACA
ACAACAACAACAACAAGAACTCACACCACCAGCACCAACCGGCCAGCTGATCCAACAAGAAAA
CCAGCTGCCGCTGCCACAACAAGGAAAAATATGAAGATTTACCGATATTAAATACATTACCGTCAGG
ACCAGAGTTGAGAGATGCTATAATGGCAGCTAAGGGAGTAGCAAATGTTACTGAATTAATTGATCG
AATTAATAATCATCGTGTAAAATCGATGCACCATCGACAAAACACCATCATGAATTGAACAAACC
AAATCTGACAAAGTAGTTGAGGATGAAGTTGAAGTTTCTGATAATGCCTCTATTGATTCTACTAA
TGGTGACGATTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTACGGTTGATCCCATGGT
TAGTGAAGTTTATGACAAGTTGTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C_homolog 1364aa (SEQ ID NO 452)

MTSNSPPLGSTTNDQRLPQSGVSSIPTNKLPLPNANEDFATGVSNQDQDVLFRGKSKKLGGKMMANN
NANKDERKNSHGNIKNSEKTTAKPNETKHESNGEKLEFNVPKSVMPKHTSSGNPKAPTNGQISNV
TPSQPSPKQTTSGSTNANDIPPISPKQPEKASKLNKLKIGRSRSSASTVVPSSSTASTTTNPGDP
KSQPKRRSSSFNFVTPSLTSDLAYDDPALVSQLSNNSNSNSSSPNVSRNSKKGGLFSSLSKFR
SSSASSKQPQSHSSPTSTTTTNGGNSAAPKSSSHSPKFNPSLVGPVSKHNREEDLVSLTNL
PAGSGIPIKRPISIGNSIFKDSFLDDASSPSSSLNSDGLKFFRRRSSVASTPSTHASTPVL
NKNPNRRKVPIEEISEVRLRRVTFVSKLEHDPQQQIPSRPKRGNVLIPQDINAPPPRLCLGISV

NEPNNKDDGKSHNHSKYSDEHIALAEDAQRRAIIEAEKHAQEAHRQAKKIAQEVSGYRSHRFISIK
EGGSVGNSTNGNDNDEDDDEVEEAVDKKLANDVSDGPLHVHEQHFEIEIESKTGEKTISLETIY
TRCCHLREILPIPATLKQLKNKTAPLEVLKMLNPKPTLIDVLSFSDFIAITPINTVIFDNVTMTTE
MLKNFLGSLTYNKQLEKLSLRNVSIDELGWKYLCEFLATNKTVKKLDISQORIKPDTPTDSIRGNM
NWDLFIRSLILRGGIEELVINGCKLSDAIFEKFINQAVKKSTYRLGIAGIDLNVKKSEMVTSWLT
GNSQCVGVDFIANDLSKGQLRPFINAFNTGKVNVLVFFSLNSTNLSNIEETSDLIKSLINVKTLRF
LDLSSIPNIFPKIITHLDKYLPRYPNLRRIHFDLNELTAQAIGSLAGCLSKMPQLVHVSLLGNRNL
STTSAATLYGAVKQSKTLFALDLDYDLIPDQLSQRIAFYLMRNLEYTLKPSHGGNIESNPEKPEDL
MYDGSLLMETAEKLLVEIEKGKKEDIKMORIISDSVLERTSIRKDIHKTIDTLFEQRNLGKLSFE
GKENLVRFCLLDSSLEKLVVMVEEHANGLLLTPTTSTDDLRSRAMSPSVTVDTIHESANELITAGP
ILSPHVNRAEQSSYFPVFANNDNLTPHQVVVESNDEGRDVPIDKMTGRPVLI RTSISQTSVHAKEQ
EIEEGELHKFGFFIQKERQKQQQQQQQQQNSHHQHQAQSIQQENQSPSPQQGYEDLPILNTLP
SGPELRDAIMAAKGVANVTELIDRINNHRVKIDAPSTKHHHELNKPNSDKVVEDEVEVSDNASIDS
TNGDDLHLQLDGKGHNGTVDPMVSEVYDKLLNDAERVRSNRDI

YPL175W_homolog 1859bp public: 1..393/395..1859, PathoSeq:

394;CDS: 501..1856 (SEQ ID NO 453)

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AATTCAATGTAGGTGATATCACTTTCTGAGAGTTCTTATTACGATATATAAAATACATAGCCAAAA
TTATAATGAAGTAAAAACATGTAACGTGTGAATTTTATTCAAGTCCAAAGGTATTGATTAATATTG
TAGAGTGTGAGCATTTAAATATGAAGGAAGACCGATAACCTAAAGTTTCTCAGGGTGTCGAA
GGCTAGGAGGAATAAAATCTGAGTAGAGAACTTTCTGTTTATATCAGTTTTTTGCAAGAAAAAAGG
AAAACAAAACAAAATAACACCAACCAACGAATTACACAAGCACATCCTAAACACCACTCTGTTGGAG
CACCAATCAACCTGAGAAATGCAAACTTGTAATAAAATATGGGATACAATATAGCAATGGTAACAG
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AACTAGGACACTCAGTGGTTATCATAACTCATAATTATTCATCAAGAAATGGTGTACGAGTATTAA
CGAATGGTTTGAAAGTGTATTATGTACCCTTTGGGTGATCTATAGAAGCTCAGTTTTTCCCAACTG
TATTTCTGTGCTTCCCAATATTGAGGAATATCTTCATACGAGAAAACATTGAGATTATTCACGGAC
ATGGTTCTTTCAGCACATTATGCCACGAAGCTATATTACATGGCCGAACAATGGGATTAAAAACAG
TCTTCACTGATCATTCACTTTTTGGATTGCGGAGATTGGATCAATTATGGGGAATAAAGCATTA
AGTTCACTTTCACTGATGTTGGCCATGTTATCTGTGTCAGTCACACCTGTAAAGAAACACGGTTT
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AGCCCAAATCGCATTGTGTGAACAAGAACTATACTAAAGAGATCACCATTGTGGTGATCACGAGAT
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AAGTGAAATTTCTAATTGCTGGTGACGGCCCCAAGTTTTTAGATTTAGAACAAATGAGAGAAAAGT
ACTTTCTTCAGGAAAGGGTTACATTAGTAGGCGCTATAAAACACGAAGAAAGTAAGAGATGTAATGG
TCCAAGGTGACATATACTTACATCCTTCATTAACAGAGGCGTTTGGTACAGTTATTGTGGAAGCTG
CATCATGTGGGTTATATGTTGTCACTACAAAAGTTGGAGGCATACCCGAAGTCTTACCAAACGAAA
TGACAAGCTTTGCTGAACCGGAAGAAAACCTCACTTATTGATGCTGCTATAGATGCTATAAATAAAA
TTGAAAGTAATGAAATCGATACCTCAAAATTTACGATGCGGTTGCAAAAGATGTACAGTTGGAATG
ATATTGCAAGAAGAACAGAAAATGTTTATAATTCACCTTGATTTAGACAAACTAAACGAGTCTTTAC
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TAGTGGATATTTTTATTTTCGTGATACTAGAATGGTTGTATCCCGCTGATCATATCGATAAAGCAA
CAAAATGGCCACTGGCTATCAAGGAAGAAGACGAGCTGGAAGAAGAAACATTTATTTTTCCGAACA
AAGTAAATTAG

YPL175W_homolog 452aa (SEQ ID NO 454)

MGYNIAMVTDFFYPQPGGVEFHVYHLSQKLIELGHSVVIITHNYSSRNQVRVLTNGLKVYYVPLWV
IYRSSVFPTVFSFPILRNIFIRENIEIIHGHGSFSTLCHEAILHGRTMGLKTVFTDHSFLGFAEI
GSIMGNKALKFTFSDVGHVICVSHCKENTVLRGSIDPIKVSVIPNAVISKDFKPKSHCVNKNYTK
EITIVVITRLFPNKGADLLTAVIPKICQLKPKVKFLIAGDGPKFLDLEQMREKYFLQERVTLVGA
KHAEVRDVMVQGDIIYLHPSLTEAFGTVIVEAASCGLYVVTTKVGGIPEVLPNEMTSFAEPEENSLI
DAAIDAINKIESNEIDTSKFHDAVAKMYSWNDRRTENVYNSLDLCLKLNESSLHLRLQRYCCGII
AGKLYALCVIVDIFIFVILEWLYPADHIDKATKWPSAIKEEDESEETTFIFPNKVN

YPL218W_homolog 1231bp PathoSeq: 1..407, public: 408..1231; exon 1: 501..518, intron 1: 519..676, exon 2: 677-1228 (SEQ ID NO 455)
GATACAATTCACGACCTCTAATTTCCCTTAGTGATAGGTTAATCATGAAATATATAAAATGTCTAGA
AATAATTGAATAATGATATAAATATAATGTTGTGAAACTTGTGAAAAATTTGACAGCCTAGTAAC
TCAAGTGTGTGTTACACTCTTGTATTATTATTATTATATCGTTTACAAGTAGATTTCTCATTTTGA
ACAGCAAATACTGTCGTTAATAGGAATCAGAGGCAGAAAGAAAGAGAGAGAAAAAAGGACA
CATTTACACGTACACCCTTAACCTGAAGGAAAAAACAACAAGAGAGACAAAGAAAGAGACAAA
GAAAATACTTTCAACAACGAAAGATTGAGATATTGGTGATTTTCACAAACCAAAAAAAGAATAC
ACAACCTGTAGATTAACAGAATTTGAACATTTCTAGAGTTTCTTATATTTCCCCCAAGGTGGACAA
TTAATAATAACATTTTGATTATACAAGAACATTTCAATCATGTGGATTTTGTGCTGGTGTATGTAAT
GATTTATCTTTACCGAATCAATACTTTATTTATGAGTGATTGGTTGGTTGGTTATAATACCACCAC
TTTATTTCTATTAACCAAGTTTGATCTAATTACTGATCTGTATATACTAACCAAATATTTACCTTAT
CACTTAATTATTTACAGTTCAAGATATATTATCATCATTAGGATTATGGAATAAACATGCCAAATT
ATTATTTTGTAGGGTTAGATAATGCTGGTAAACTACTCTTTTACATATGTTAAAGAAATGATAGATT
GGCCACTTTACAACCAACATTACATCCAACCTCAGAAGAATTGGCCATTGGATCAGTTAGATTTAC
TACTTTTGATTTAGGTGGACATCAACAAGCTAGAAGATTATGGAAAGATTATTTCCCTGAAGTCAA
TGATATTGCTCTTTTAGTTCGATGCTGCTGATACCGAAAGATTGCTGAATCCAAAGCTGAATTGGA
AAGTTTATTTAGAATTGAAGAATTGAGTCAAGTTCCATTTGTTATTTTGGGTAATAAGATTGATGT
TCCTACTGCAGTAGGGGAAATGGAATTGAAAAATGCCCTTGATTATATAACTACTGGTAAAGA
TACTGGTAAATTGCCTGAAGGTACTAGACCAATTGAAGTGTATGTTTCCGTTGTTATGAGATC
TGGATATGGTGAAGCCTTCAATGGTTATCACAATACATTTAA

YPL218W_homolog 190aa (SEQ ID NO 456)
MWIFDWVQDILSSLGLWNKHAKLLFLGLDNAGKTTLLHMLKNDRLATLQPTLHPTSEELAIGSVRF
TTFDLGGHQARRLWKDYFPEVNGIVFLVDAADTERFAESKAELESLEFRIEELSQVPFVILGNKID
VPTAVGEMELKNALGLYNTTGKDTGKLEPGRPIEVFMVSVVMRSGYGEAFKWLSQYI

YOL127W_homolog 429 bp, public: 1..429, CDS: <1..429 (SEQ ID NO 475)
CTTATAGCAACTACTAAAGCTTCAGCTGCTAAAAAGCTGCTTTGAAAGGTGTTAACGGTAAAAAG
GCTTTAAAAGTTAGAACTAGTACTACTTTTCAGATTACCAAAAACCTTAAAATTAACAGATCTCCA
AAATACCAAAGAAAATCAGTCCACACTACACAGATTGGATGCCACAAAATCATTTGTTGCTCCA
ATTGCCACTGAACTGCTATGAAAAAGTCGAAGATGGTAACACTTTGGTTTTCCAAGTTGACATC
AAATCCAACAAACACCAAATCAAATCTGCTGTTAAAGAATTATACGATGTTGATGCCTTATACGTT
AACACTTTGATCAGACCTAACGGTACCAAGAAAGCTTACATCAGATTAACCTCTGACTACGATGCT
TTGGATATTGCTAACAGAATCGGTTACATCTAA

YOL127W_homolog 142 aa (SEQ ID NO 476)
LIATTKASAAKKAALKGVNGKKALKVRTSTTFRLPKTLKLTRSPKYQRKSVPHYNRLDAHKIIVAP
IATETAMKKVEDGNTLVFQVDIKSNKHQIKSAVKELYDVALYVNTLIRPNGTKKAYIRLTSYDA
LDIANRIGYI

YJL188C_homolog 117 bp public: 1..117, CDS: <1..>117 (SEQ ID NO 477)
TTAGATACCCAACCTTAGTTCTTCTCCAGTGTCTTCTTTTAGCATTGTATCTGATTTTGTGTGTCAGT
TCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTTTGAGCCTTAGC

YJL188C_homolog 39 aa (SEQ ID NO 478)
LDTQLSSSPVSSFSIVSDFVSSQSDPLWQWSVLLLSLS

YGR183C_homolog 198 bp public: 1..198, CDS: 1..198 (SEQ ID NO 479)
ATGTTGACAGTCCTTGGTCGTTTACTTGAAAGAACTCAATCTACGTTGCCACTATCTTTGGCGGT
GCTTTTGGCTTTCCAAGGTTTTTTTCGATGTTGCAGTGAACAAATGGTGGGAGGAACACAACAAAGCT
AAATTATGAAAAACGTCAAAGGAAAATTCCTTGAAGGTGAAGGTGAAGAAGAAGATGACGAATAA

YGR183C_homolog 65 aa (SEQ ID NO 480)

MLTVLGRLLEARNISYVATIFGGAFQGFDFDAVNKWWEHNKAKLWKNVKGKFLEGEGEEDDE*

YDR529C_homolog 457 bp Pathoseq: 1..457, CDS: 1..457 (SEQ ID NO 481)

ATGGTTCAATCTATGACATCTGTCGTTAAGGCAGCTAATTTTCATTTTAGCAAGACCAACATTATCA
AAAATCATTTACACCACTTGCTCAAAAATTCAC TGCTTATGCAGGGTATAGAGAAATGGGATTAAAA
TTCAATGATTTACTTCTTGAAGAAACCCCAATTATGCAAAC TGCTATTTAAAAGATTACCTTCAGAA
TTAAATTATTTCAAGAAATTTTAGAATTTCTACTGCTCATCAATTAGCTTTATCTCATCAATTATTA
CCAGCTGAAAAAGCTGTTAAACCTGAAGAAGATGATAATTATTTGATTCCTTATATTTTAGAAGCT
GAAAAAGGAAGCTTTTGAAGAAAGCTGTATTGGGGAATATTGACGCTAGTGCGATTGTAATTAATACG
ACGAATAAGAAACGGACGAGGAAGAGGAAGAAGATGAGAAGGTCAAACATTGAAATATGAA

YDR529C_homolog 151 aa (SEQ ID NO 482)

MVQSMTSVVKAANFILARPTLSKIITPLAQKFTAYAGYREMGLKFNDLLLEETPIMQTAIKRLPSE
LNYSRNFRI LTAHQ LALSHQL LPAEKAVKPEEDDNYLIPYILEAEKEAFEKAVLGNIDASAIVINT
TNKKRTRKRKKMRRSNIEI

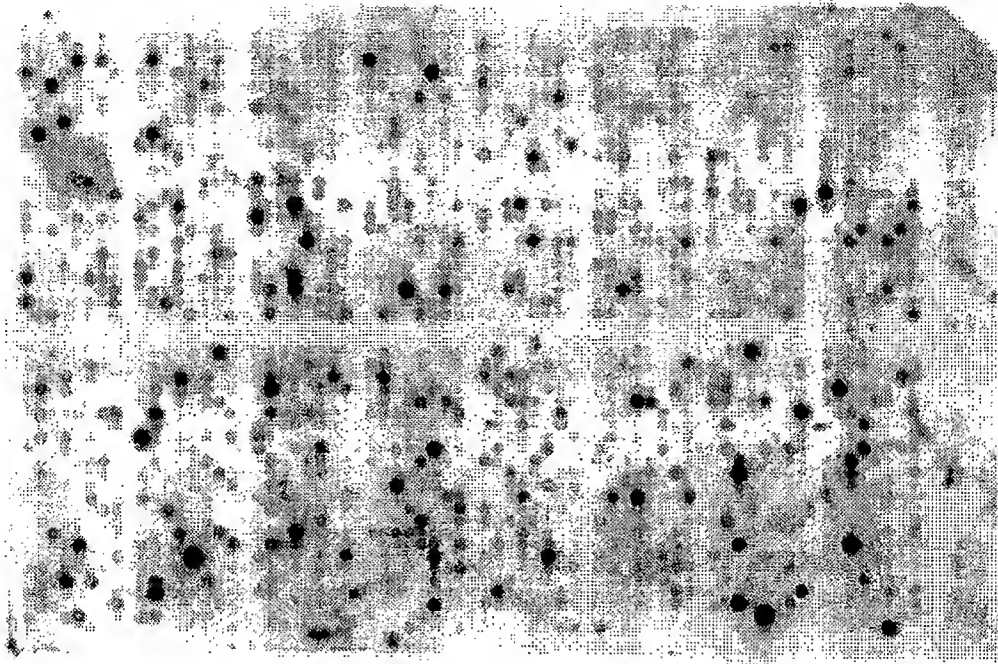
YBL003C_YDR225W_homolog 399 bp public: 1..399, CDS: 1..399 (SEQ ID NO 483)

CTACAATTCTTGAGAAGCCTTAACACCACCTTTACCTGATTTCTTTGGCAACAAGTTTGTATGGAT
GTTTGGTAACACACCACCTTGGGCGATGGTGACATCACCCAACAATTTGTTTAATTCCTTCATCATT
TCTGATGGCCAATTGTAAGTGTCTTGGGATTATTTCTGGATTTCTTGTTGTCTCTGGCAGCGTTACC
AGCTAATTCCAAAATTTTACGACGCTAAATATTTCCAAGACTGAAGTCAAGTACACTGGAGCACCAGA
ACCGATTCTCTGAGCGTAGTTACCTTTTCTTAACAATCTGTGGACTCTACCGACTGGGAAAGTCAA
ACCAGCTTTGGCTGATCTTGAAGTTGAAGCTTTTTCGGAAGTTCCTGCTTTACCTTTACCACCTGA
CAT

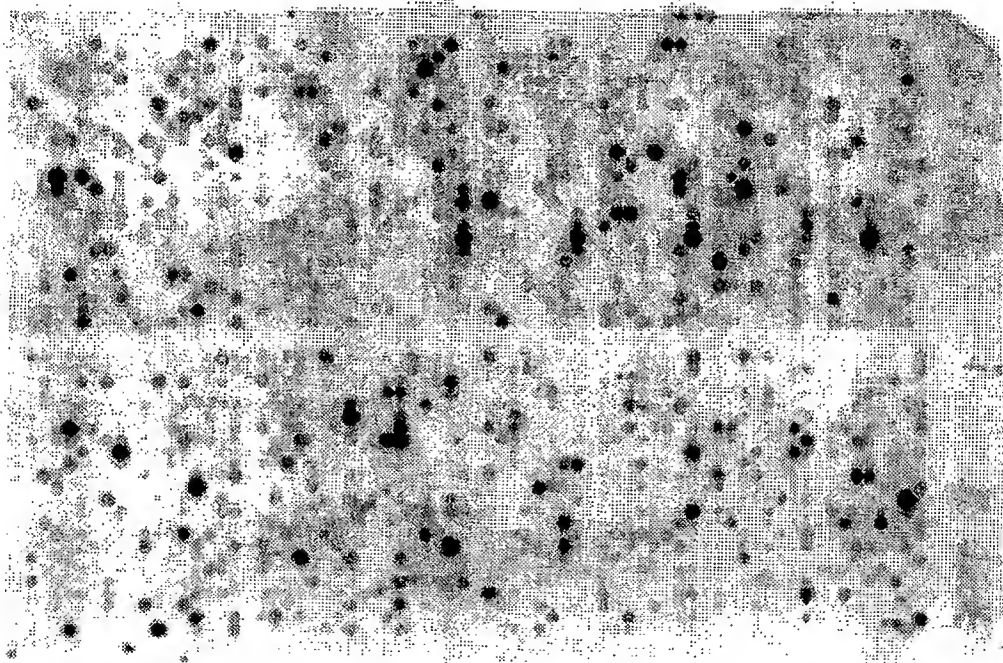
YBL003C_YDR225W_homolog 132 aa (SEQ ID NO 484)

MSGGKGKAGTSEKASTSRSAKAGLTFFVGRVHRLLRKGNYAQRIGSGAPVYLTSVLEYLAAEILEL
AGNAARDNKKSR IIPRHLQLAIRNDEELNKL LGDVTIAQGGVLPNIHQNL LPPKSGKGGVKASQEL

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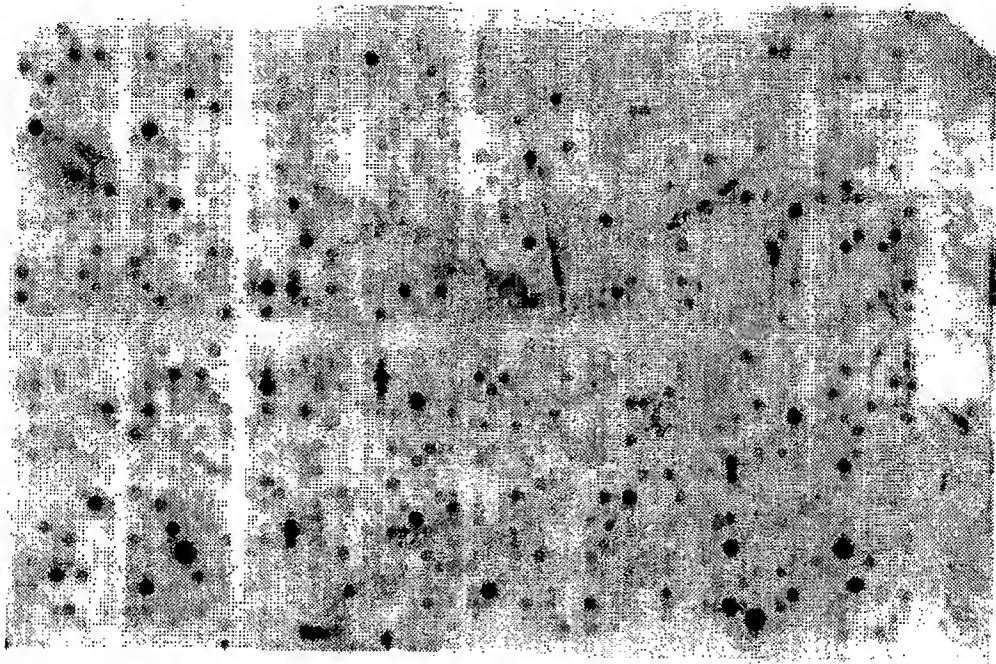
Filter I



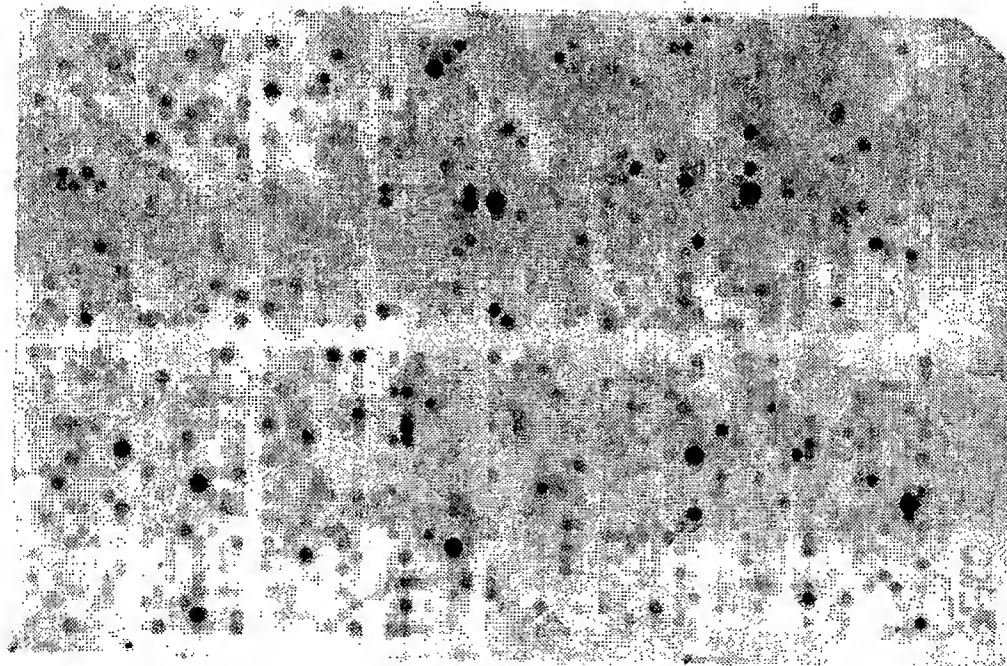
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FIG. 3A

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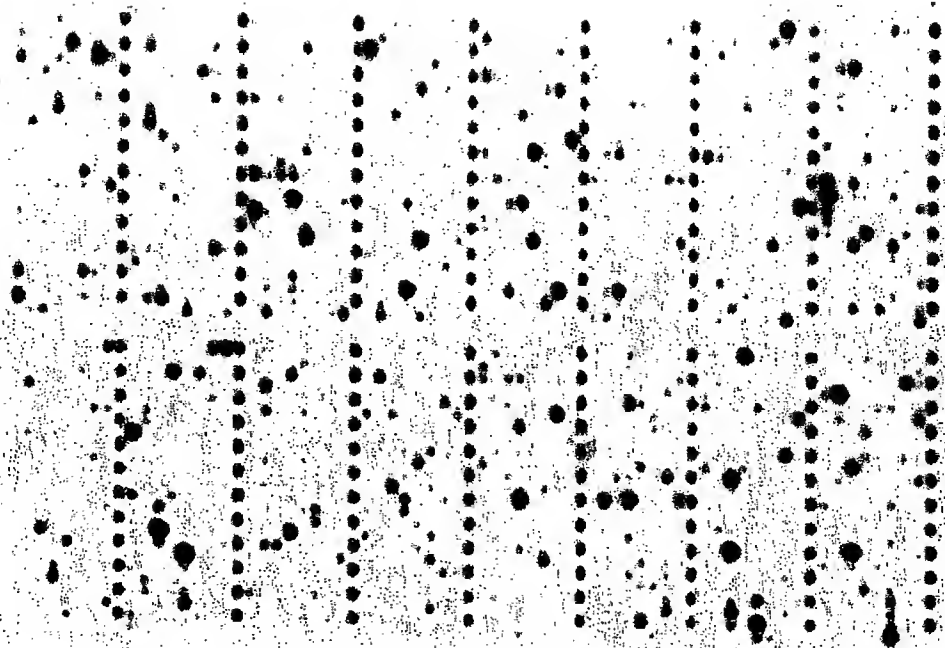
Filter I



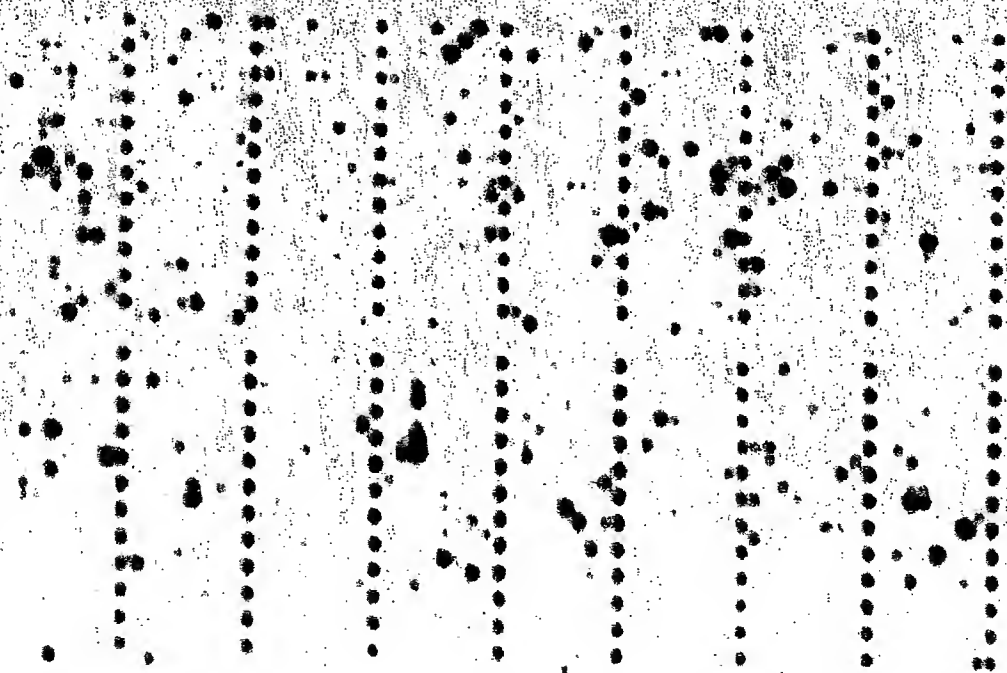
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FIG. 3B

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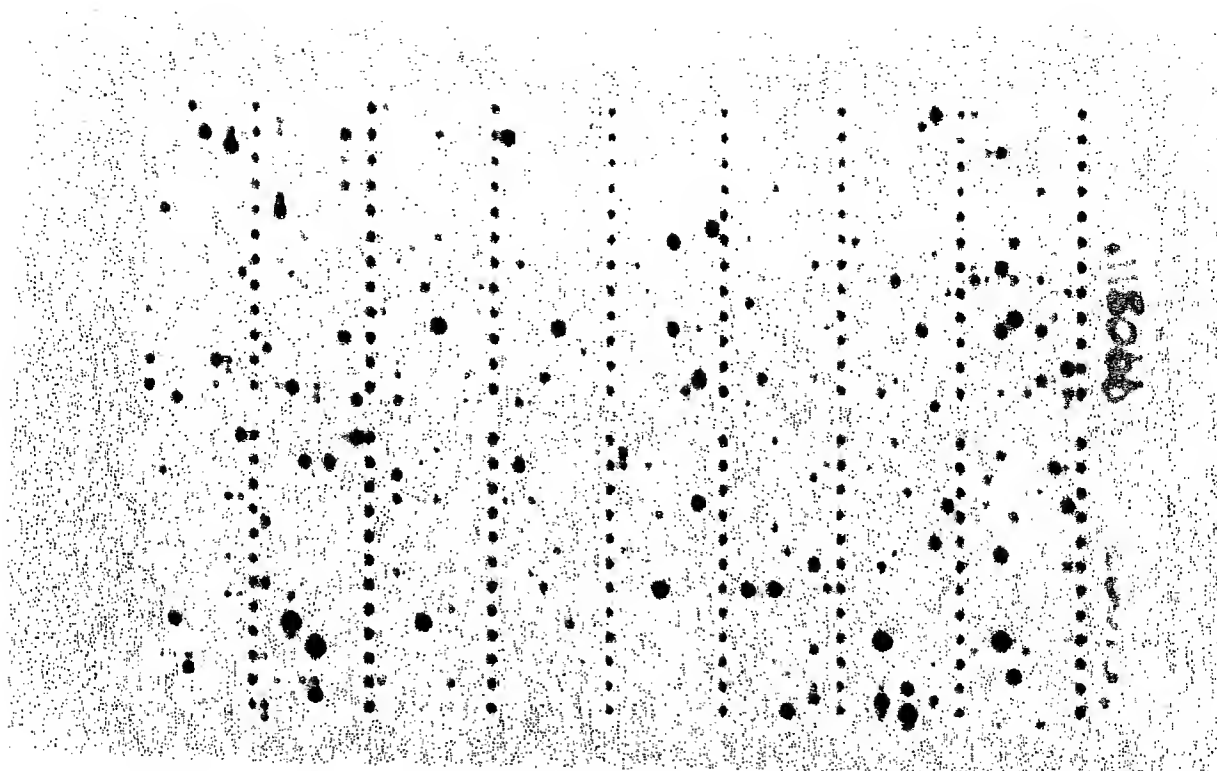
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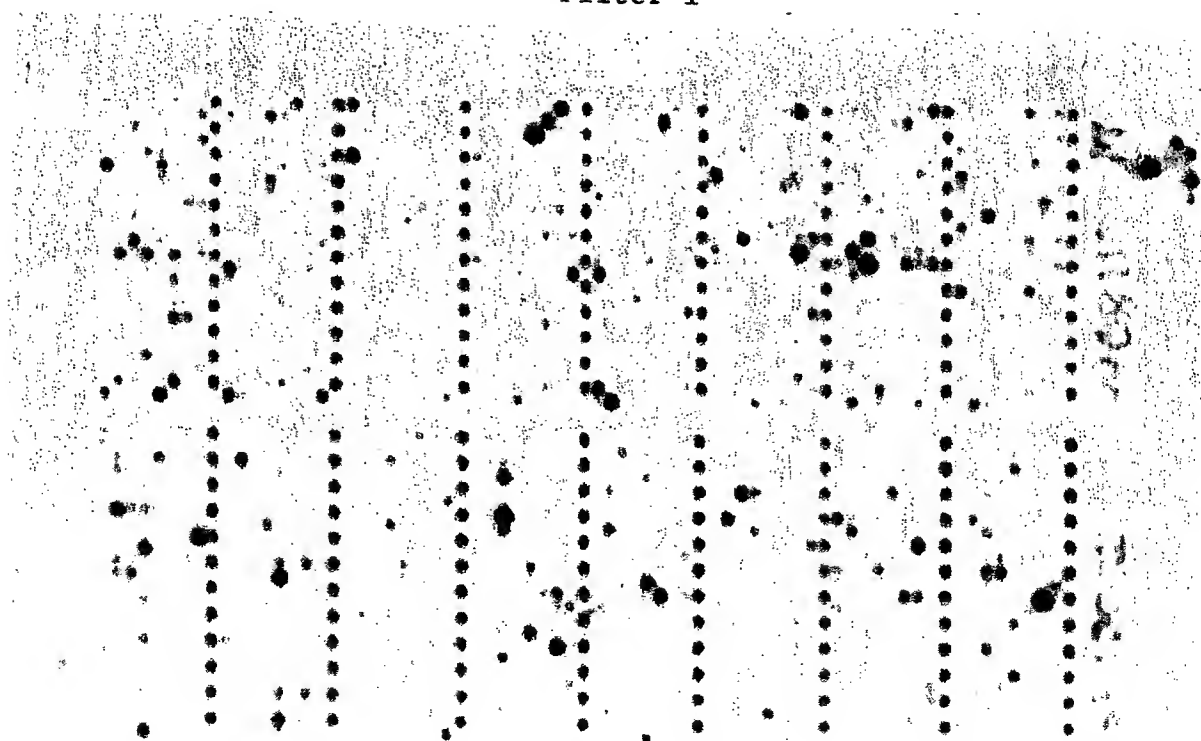
Filter II

FIG. 4A

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Filter I



Filter II

FIG. 4B